

Table 1

1	2	3	4	5	6	7	8	9	10	11	12	13
Seq ID	CuraGen sequence ID	Base pos. of SNP	Polymorphic sequence	Base before	Base after	Amino acid before	Amino acid after	Type of change	Protein classification of CuraGen gene	Name of protein identified following a BLASTX analysis of the CuraGen sequence	Similarity (pValue) following a BLASTX analysis	Map location
1	cg43921971	1030	GGGTTTGATTG GCGCACCAAGA TC[T/C]CCAACA GCCAGTGTGTG TTTCCCAT	T	C			SILENT- NONCODING	apoptosis	Human Gene Similar to SWISSPROT-ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa.	6.10E-68	
3	cg43314087	475	ATGGGTTTTTTT GTTTTGTTTTT G[T/gap]TTTTTTT TTAAAGGCAAG GGGTCT	T	gap			SILENT- NONCODING	ATPase-associated	Human Gene SWISSPROT-ID:P14415 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) - HOMO SAPIENS (HUMAN), 290 aa.	4.00E-160	17 (17p)
4	cg43314087	484	TTTGTTTTTGTTT TTGTTTTTTTTT T[gap]AAAGGCA AAGGGGTCTGA AGAGATG	T	gap			SILENT- NONCODING	ATPase-associated	Human Gene SWISSPROT-ID:P14415 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) - HOMO SAPIENS (HUMAN), 290 aa.	4.00E-160	17 (17p)
5	cg43132502	200	CATGAGGTGGC ACGAGGCAGGA GTT[G/gap]GCGA TGCCACCTGGG GGTCACATTG	G	gap			SILENT- NONCODING	ATPase-associated	Human Gene Similar to SPTREMBL-ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa.	9.40E-58	11
6	cg43988460	4698	ACATAATTGTGA CCAAAAA A[A/gap]GAAAGG AAAGAAAGGGG TGGCCTGA	A	gap			SILENT- NONCODING	cadherin	Human Gene SWISSPROT-ID:P19022 NEURAL-CADHERIN PRECURSOR (N-CADHERIN) - HOMO SAPIENS (HUMAN), 906 aa.	0.00E+00	18 (18q11.2)

7	cg43988460	4708	TACCAAAAAAAAA AAAGGAAAGGAA A[G/A]AAAGGG TGGCCTGACACT GGTGGC	G	A				SILENT- NONCODING	cadherin	Human Gene SWISSPROT- ID:P19022 NEURAL-CADHERIN PRECURSOR (N-CADHERIN) - HOMO SAPIENS (HUMAN), 906 aa.	0.00E+00	18 (18q11.2)
8	cg43982945	460	GACACATGTCAG GCTGGGCGAGC AG[C/gap]CACTC TGATCAGCACCA GGTCCCCGA	C	gap				SILENT- NONCODING	cathepsin	Human Gene Similar to SWISSPROT- ID:Q26534 CATHEPSIN L PRECURSOR (EC 3.4.22.15) (SMCL1) - SCHISTOSOMA MANSONI (BLOOD FLUKE), 319 aa.	2.00E-80	11
9	cg43266931	96	GGGCGCTAGCG GGGGTGACACGG CGG[G/gap]CCG GTAGGCCGCCA GGATCTCGGGC	G	gap				SILENT- NONCODING	chloride_ channel	Human Gene Similar to SWISSNEW- ID:O15247 CHLORIDE INTRACELLULAR CHANNEL PROTEIN 2 (XAP121) - HOMO SAPIENS (HUMAN), 243 aa. pcds:SWISSPROT-ID:O15247 CHLORIDE INTRACELLULAR CHANNEL PROTEIN 2 (XAP121) - HOMO SAPIENS (HUMAN), 243 aa.	3.10E-59	9
10	cg43321451	1126	GAAGGCACACA CACACACACACA CA[C/gap]AGCAA AAGCTAAATCAT CACCCGCG	C	gap				SILENT- NONCODING	collagen	Human Gene SWISSPROT- ID:Q99715 COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3063 aa. pcds:SPTREMBL-ID:Q99715 COLLAGEN TYPE XII ALPHA-1 PRECURSOR - HOMO SAPIENS (HUMAN), 3063 aa.	0.00E+00	6
11	cg43933757	3195	TCATCTCCCTGC AACCTCCGCCCTC CT[C]GGGTTCA AGCGATTCTTGT GCCTCA	T	C				SILENT- NONCODING	complement	Human Gene SWISSPROT- ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa.	0.00E+00	5 (5p13)
12	cg43933757	3212	CGGCCTCCTGG GTTCAAGCGATT CTT[C]GTGCCCTC AGCCTCCCAAG CAGCTGG	T	C				SILENT- NONCODING	complement	Human Gene SWISSPROT- ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa.	0.00E+00	5 (5p13)

13	cg43933757	3346	TCCAACCTCCTGA CCTCAGGTAATC C[G/A]CCTGCCT TGGCCTCCCAAA GTGCTG	G	A				SILENT- NONCODING	complem ent	Human Gene SWISSPROT- ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa.	0.00E+00	5 (5p13)
14	cg42185571	2224	CTTAGCTCTACG ATTTAAATCCAT G[T/gap]GTCCAA GGGGGAAACA TATTATAT	T	gap				SILENT- NONCODING	complem ent	Human Gene SWISSPROT- ID:P02748 COMPLEMENT COMPONENT C9 PRECURSOR - HOMO SAPIENS (HUMAN), 559 aa.	7.70E-308	5 (5p13)
15	cg42185571	2367	TAATATAGATAG TGTCAGTAGCA G[A/gap]ATAGAA TGAACATAAACT ATTAGTT	A	gap				SILENT- NONCODING	complem ent	Human Gene SWISSPROT- ID:P02748 COMPLEMENT COMPONENT C9 PRECURSOR - HOMO SAPIENS (HUMAN), 559 aa.	7.70E-308	5 (5p13)
16	cg43947909	265	GAATTGTCAGA AGACTTGGCTCA G[C/T]TGGAGGA GCTGATAGACAT GGCTGT	C	T				SILENT- NONCODING	complem ent	Human Gene Homologous to SWISSPROT-ID:Q07021 COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN PRECURSOR (GLYCOPROTEIN GC1QBP) (GC1Q- R PROTEIN) (HYALURONAN- BINDING PROTEIN 1) (PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT) - HOMO SAPIENS (HUMAN), 282 aa.	6.9E-129	17

17	cg43143315	2860	GTGTGTGTGTCT GTGTGTGTGTGT C/C/GTGTGTATG TGTGTGTGGGTT CTAATG	C	G			SILENT- NONCODING	cyto450	Human Gene SWISSNEW-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.) (P450- CC24) (VITAMIN D(3) 24-HYDROXYLASE) (1,25-DIHYDROXYVITAMIN D(3) 24-HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.lpcis:SWISSPROT-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.) (P450- CC24) (VITAMIN D(3) 24-HYDROXYLASE) (1,25-DIHYDROXYVITAMIN D(3) 24-HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.	1.9E-279	20
18	cg43327428	1746	AGCAGGCTGGC CTATGTGGTCTA AG/A/GTTCAGC CTGAACACTCATA GACACTG	A	G			SILENT- NONCODING	cyto450	Human Gene SWISSNEW-ID:P04798 CYTOCHROME P450 1A1 (EC 1.14.14.1) (CYP1A1) (P450-P1) (P450 FORM 6) (P450-C) - HOMO SAPIENS (HUMAN), 512 aa.lpcis:SWISSPROT-ID:P04798 CYTOCHROME P450 1A1 (EC 1.14.14.1) (P450-P1) (P450 FORM 6) (P450-C) (TCDD-INDUCIBLE) - HOMO SAPIENS (HUMAN), 512 aa.	2.5E-279	15 (15q22)
19	cg32296860	376	CAGCACTTTGGG AGCCCGAGGCG GGT/CJGGATCA CCCGAGGTCAG GAGTTCGA	T	C			SILENT- NONCODING	cytochrome	Human Gene Homologous to SPTREMBL-ID:Q27524 CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) - CAENORHABDITIS ELEGANS, 1647 aa (fragment).	6.6E-124	
20	cg32296860	383	TTGGGAGGCCG AGCCGGGTGGA TCA/C/gap/CCGA GGTCAGGAGTT CGAGACCAGC	C	gap			SILENT- NONCODING	cytochrome	Human Gene Homologous to SPTREMBL-ID:Q27524 CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) - CAENORHABDITIS ELEGANS, 1647 aa (fragment).	6.6E-124	

21	cg32296860	385	GGGAGGCCGAG GCGGTGGATC ACC[C/gap]GAGG TCAGGAGTTCGA GACCAGCCT	C	gap				SILENT- NONCODING	cytochrome	Human Gene Homologous to SPTREMBL-ID:Q27524 CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) - CAENORHABDITIS ELEGANS, 1647 aa (fragment).	6.6E-124	
22	cg32296860	397	CGGGTGGATCA CCCGAGGTCAG GAG[T/A]TCGAG ACGAGCCTGGC CAACATGGT	T	A				SILENT- NONCODING	cytochrome	Human Gene Homologous to SPTREMBL-ID:Q27524 CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) - CAENORHABDITIS ELEGANS, 1647 aa (fragment).	6.60E-124	
23	cg32296860	439	CAACATGGTGAA ACCCGTGCTCTA CIT/CJAAAAATAC AAAAATTAGCTG GGTGC	T	C				SILENT- NONCODING	cytochrome	Human Gene Homologous to SPTREMBL-ID:Q27524 CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) - CAENORHABDITIS ELEGANS, 1647 aa (fragment).	6.60E-124	
24	cg43264442	199	GGGGCGCGGGT GGAGAAGCTGC GGC[A/G]GCGCG GCCCGTAGGAA GGTGCTGTC	A	G				SILENT- NONCODING	dehydrogenase	Human Gene TREMBLNEW- ID:G806944 UDP-GLUCOSE DEHYDROGENASE, UDPGDH=52 KDA SUBUNIT {EC 1.1.1.22} - BOS TAURUS, 468 aa.	8.60E-240	4
25	cg43264442	236	AGGAAGGTGCT GTCCGAACGATC GG[G/A]ATAGGA GCGGTCCCTGC GCTTGCTG	G	A				SILENT- NONCODING	dehydrogenase	Human Gene TREMBLNEW- ID:G806944 UDP-GLUCOSE DEHYDROGENASE, UDPGDH=52 KDA SUBUNIT {EC 1.1.1.22} - BOS TAURUS, 468 aa.	8.60E-240	4
26	cg43998926	130	GAACCCAAAGAG CCACTGATAACT GG[C/gap]ACAAT CCAATGAAACAG AGGAAGCA	C	gap				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT- ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa.	1.30E-190	15

27	cg43998926	560	CTCAGGCTGAGT TGCCCTCCAGTCT TTT/GIGGAATGTC ATCTTATACTGG TACTG	T	G				SILENT- NONCODING	dehydrog enase	Human Gene SWISSPROT- ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa.	1.30E-190	15
28	cg43941594	499	GGTTATAAAAAT AGATAAECTCGCA G/A/GJGTCATAAA TATCTACAGTTA GTAGA	A	G				SILENT- NONCODING	dehydrog enase	Human Gene Homologous to SWISSPROT-ID:P13707 GLYCEROL- 3-PHOSPHATE DEHYDROGENASE (NAD+), CYTOPLASMIC (EC 1.1.1.8) (GPD-C) (GPDH-C) - MUS MUSCULUS (MOUSE), 348 aa.	1.90E-137	3
29	cg43962927	462	GCCACTCCCTG CTCCCTGCCCTGA GC/G/AJCCATTC GCAGTCTTGTTT CCTGTTT	G	A				SILENT- NONCODING	dna_rna_ bind	Human Gene SWISSPROT- ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00 (11q13.2)	11
30	cg43991661	671	CTTGTTTATTATC TATCATAGACAT C/GJAGATGATC ATAGTTAATACC AATT	C	G				SILENT- NONCODING	dna_rna_ bind	Human Gene TREMBLNEW- ID:G2058493 TELOMERIC REPEAT DNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 419 aa.	5.10E-224	8
31	cg43991661	737	ACTGTTTtaggc CCAATATTGATA T/A/GJTAAATGA AGGTATCAGAGA ATCTT	A	G				SILENT- NONCODING	dna_rna_ bind	Human Gene TREMBLNEW- ID:G2058493 TELOMERIC REPEAT DNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 419 aa.	5.10E-224	8
32	cg43310449	206	CTAAAGATTTCa TGCTCTCAGTGG A/A/GJCTGGCAT ACTGTAATTGCT ATGTGG	A	G				SILENT- NONCODING	dynein	Human Gene SWISSPROT- ID:Q63100 DYNEIN INTERMEDIATE CHAIN 1, CYTOSOLIC (DH IC-1) - RATTUS NORVEGICUS (RAT), 643 aa.	1.0e-312	
33	cg43310449	231	ACTGGCATACTG TAATTGCTATGT G/G/AJAACTTAAT ATAACCTCAACA GCAGC	G	A				SILENT- NONCODING	dynein	Human Gene SWISSPROT- ID:Q63100 DYNEIN INTERMEDIATE CHAIN 1, CYTOSOLIC (DH IC-1) - RATTUS NORVEGICUS (RAT), 643 aa.	1.0e-312	

34	cg43984524	1227	TCAATGAGGCTT TCTATTAATTCC [T/C]TTAAAGCA ATGGTTATTATT GAAA	T	C				SILENT- NONCODING	esterase	Human Gene Similar to SPTREMBL- ID:P70665 SIALIC ACID-SPECIFIC 9- O-ACETYLESTERASE - MUS MUSCULUS (MOUSE), 541 aa.	3.2E-99	
35	cg43248101	2516	GGCCCTGAATGT TATGAAGGTTTG AIG[AG]TCAGCC TACAGATAACAG GATTAT	G	A				SILENT- NONCODING	fgf	Human Gene Homologous to SWISSPROT-ID:P21781 KERATINOCYTE GROWTH FACTOR PRECURSOR (KGF) (FIBROBLAST GROWTH FACTOR- 7) (FGF-7) (HBGF-7) - HOMO SAPIENS (HUMAN), 194 aa.	9.30E-106	15 (15q15)
36	cg43974968	2973	CAGTGGCTCAC GCCTATAATCCC AG[C/A]ACTTTGG GAGGCCAAGGC AGGAGGA	C	A				SILENT- NONCODING	fgf	Human Gene Homologous to SPTREMBL-ID:P78443 21 KD BASIC FIBROBLAST GROWTH FACTOR (BFGF) - HOMO SAPIENS (HUMAN), 196 aa.	1.70E-103	4 (Xq26)
37	cg43074195	222	CAGCTGAAGGA GATAATTGGTG GA[A/G]CAGAA CTGAAAGCTTCT AATGGAG	A	G				SILENT- NONCODING	glycoprot ein	Human Gene SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	1.40E-197	1
38	cg43074195	237	ATTGGTGTGAAC AGAAAGCTGAAAG C[T/A]TCTAATGG AGACACTCCTAC ACATG	T	A				SILENT- NONCODING	glycoprot ein	Human Gene SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	1.40E-197	1
39	cg43074195	246	AACAGAAGCTGA AAGCTTCTAATG G[A/G]GACACTC CTACACATGAAG ACTTGA	A	G				SILENT- NONCODING	glycoprot ein	Human Gene SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	1.40E-197	1
40	cg43074195	255	TGAAAGCTTCTA ATGGAGACACTC C[T/A]ACACATGA AGACTTGACCAA GAACA	T	A				SILENT- NONCODING	glycoprot ein	Human Gene SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	1.40E-197	1

41	cg43988092	658	TAGCGATACAAA TATATATATAT [A/gap]TTTATCCA AAAATATGTTTTA TACA	A	gap				SILENT- NONCODING	glycoprot ein	Human Gene SWISSPROT- ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4E-192	8
42	cg43953517	2457	AAGTTCTTG TAG TAGGTAGGGG TA[C/T]TACTAGG GATATCTGTGGC ATGATT	C	T				SILENT- NONCODING	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa.	2.9E-150	4
43	cg43953517	2464	TGTAGTAGGTAG GGGGTACTACTA G[G/C]GATATCT GTGGCATGATT TGCATT	G	C				SILENT- NONCODING	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa.	2.9E-150	4
44	cg43953517	2491	ATATCTGTGGCA TGATTATGCATT C[C/gap]GTAGTA TTATTTAAATTAAT TTGGGG	C	gap				SILENT- NONCODING	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa.	2.9E-150	4
45	cg43953517	2517	GTAGTATTATTTA ATTAATTTGGGG T/G]TCATTTTGCT TCCTTTTCTTTAT GC	T	G				SILENT- NONCODING	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa.	2.9E-150	4
46	cg43953517	2529	AATTAATTTGGG GTTCAATTTTGCT T[C/gap]CTTTTCT TTATGCTTAGAT TATCTT	C	gap				SILENT- NONCODING	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa.	2.9E-150	4
47	cg43953517	2530	ATTAATTTGGGG TTCATTTTGCTTC [C/gap]TTTTCTTT ATGCTTAGATTA TCTTA	C	gap				SILENT- NONCODING	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa.	2.9E-150	4
48	cg43290087	1150	CCTAACCTCTTG GTAACGGTAGTC CT/C]GAGAGTT CGCAGTGTCACT GAAATC	T	C				SILENT- NONCODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P52166 MEMBRANE PROTEIN SEL-12 - CAENORHABDITIS ELEGANS, 461 aa.	1.7E-97	14 (14q24.3)

49	cg43294632	913	AGTAGAGAGTAGA GGGTAAAAGCT GG/A/GjCATTGC AAAAGGATTGGT TTAAGAA	A	G				SILENT- NONCODING	glycoprot ein	Human Gene Similar to SWISSNEW- ID:Q13361 MICROFIBRIL- ASSOCIATED GLYCOPROTEIN 2 PRECURSOR (MAGP-2) (MP25) - HOMO SAPIENS (HUMAN), 173 aa. pcis:SWISSPROT-ID:Q13361 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 2 PRECURSOR (MAGP-2) - HOMO SAPIENS (HUMAN), 173 aa.	4.3E-92	12
50	cg43056971	884	GTTATTTGAAAA ATACCTATTTTT [T/gap]CCAAAGT GTGTAAAAGATT GTTTTG	T	gap				SILENT- NONCODING	glycoprot ein	Human Gene Similar to SPTREMBL- ID:O04711 P-GLYCOPROTEIN-2 - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 1233 aa.	2.2E-72	1
51	cg43976227	212	TTCATGTGCAAG CTAAGTTATTCC T[C/A]TGGTCAAT CCTCTCCATCTT CTGGT	C	A				SILENT- NONCODING	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	2.6E-60	18
52	cg43994600	1782	CCTTGTTCCAC TCTCCTTCATAT C[C/T]AAGTCATC AAACATCTGAAT GAGAG	C	T				SILENT- NONCODING	helicase	Human Gene Similar to SWISSNEW- ID:O70133 ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II) (DEAD BOX PROTEIN 9) (MHEL-5) - MUS MUSCULUS (MOUSE), 1380 aa. pcis:TREMBLNEW-ID:G2961456 RNA HELICASE A - MUS MUSCULUS (MOUSE), 1380 aa.	8.7E-67	14

53	cg43925670	2481	ATGTTCTTGTTATTT TTTTCCCATCT[T/C]TACAGACAT AAGTGAGCCTCA CTGG	T	C				SILENT- NONCODING	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0	1
54	cg43925670	2488	TGATTTTTTTCC CATCTTTACAGA[C/T]ATAAGTGAG CCTCACTGGAAA TTTT	C	T				SILENT- NONCODING	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0	1
55	cg43925670	2501	CATCTTTACAGA CATAAGTGAGCC T[C/T]ACTGGAAA TTTTTCAACAGT AGTC	C	T				SILENT- NONCODING	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0	1

56	cg43925670	2507	TACAGACATAAG TGAGCCTCACTG G A/G AATTTTT CAACAGTAGTCC AGATC	A	G				SILENT- NONCODING	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0	1
57	cg43925670	2513	CATAAGTGAGCC TCACTGGAAATT TTT/C TTCAACAG TAGTCCAGATCT TGAGA	T	C				SILENT- NONCODING	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0	1
58	cg43925670	2551	CCAGATCTTGAG ATCTTCAGAAAT G C/T AGGAATC AATGCTTATTG TGTGAG	C	T				SILENT- NONCODING	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0	1

59	cg42489232	2434	ATTTTAGTAGA GACAAGGTTTTG C/C/TATGTTGGC CAGGCTGGTCT CGAACT	C	T				SILENT- NONCODING	interferon	Human Gene SWISSPROT- ID:P48551 INTERFERON- ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA- REC) (TYPE I INTERFERON RECEPTOR) (IFN-R) (INTERFERON ALPHA/BETA RECEPTOR- 2) - HOMO SAPIENS (HUMAN), 515 aa.	3.9E-281	21 (21q22.1)
60	cg42489232	2441	GTAGAGACAAG GTTTTGCCATGT TG[G/C]CCAGGC TGGTCTCGAACT CCTGACC	G	C				SILENT- NONCODING	interferon	Human Gene SWISSPROT- ID:P48551 INTERFERON- ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA- REC) (TYPE I INTERFERON RECEPTOR) (IFN-R) (INTERFERON ALPHA/BETA RECEPTOR- 2) - HOMO SAPIENS (HUMAN), 515 aa.	3.9E-281	21 (21q22.1)
61	cg42489232	2454	TTTGCCATGTTG GCCAGGCTGGT CTC/TGAACTCC TGACCTCAAGCG ATCCGC	C	T				SILENT- NONCODING	interferon	Human Gene SWISSPROT- ID:P48551 INTERFERON- ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA- REC) (TYPE I INTERFERON RECEPTOR) (IFN-R) (INTERFERON ALPHA/BETA RECEPTOR- 2) - HOMO SAPIENS (HUMAN), 515 aa.	3.9E-281	21 (21q22.1)
62	cg43926168	694	GAAGGGCTCTC CTTCACGGGGA CTG[A/gap]AAAA AAAAAATCATGA AATCCTAAT	A	gap				SILENT- NONCODING	interleukin receptor	Human Gene Similar to SWISSPROT- ID:P18510 INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (ICIL- 1RA) (IRAP) - HOMO SAPIENS (HUMAN), 177 aa.	8.8E-94	2 (2q14.2)
63	cg43926168	704	CCTTCACGGGG ACTGAAAAAAA AA[A/gap]TCATG AAATCCTAATTTT CATTTTC	A	gap				SILENT- NONCODING	interleukin receptor	Human Gene Similar to SWISSPROT- ID:P18510 INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (ICIL- 1RA) (IRAP) - HOMO SAPIENS (HUMAN), 177 aa.	8.8E-94	2 (2q14.2)

64	cg43336163	2889	AGCCGGGAATG CTGCTGCTGCTG CT[G/A]CTGCTG CTGCTGCTGCTG GGGGGAT	G	A				SILENT- NONCODING	kinase	Human Gene TREMBLNEW- ID:G300258 MYOTONIC DYSTROPHY KINASE, DM-KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0	19
65	cg43987164	1043	AGGGCAGCCCC TCAGAAAGCCCTTC CC[G/A]GCAGAT CCGGGGACCCCC GTTCTGGT	G	A				SILENT- NONCODING	kinase	Human Gene TREMBLNEW- ID:D1023392 INOSITOL 1,4,5- TRISPHOSPHATE 3-KINASE ISOENZYME (EC 2.7.1.127) - HOMO SAPIENS (HUMAN), 604 aa (fragment).	1.3E-307	
66	cg43119489	2227	TTTTTCATCCTAT CAATTGAATGTG[G/C]CTTGAAAAA TCCAGCAAGAG CGGGG	G	C				SILENT- NONCODING	kinase	Human Gene SWISSPROT- ID:Q00537 SERINE/THREONINE- PROTEIN KINASE PCTAIRE-2 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 523 aa.	2.7E-282	
67	cg43957170	2164	CTACTAAAAATA CAAAAAATTAGC C[G/A]GGCGTGG TGGCGCATGCC TGTAGTC	G	A				SILENT- NONCODING	kinase	Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa.	1.7E-234	
68	cg43957170	2175	ACAAAAAATTAG CCGGGCGTGGT GG[C/T]GCATGC CTGTAGTCCCAG CTACTCG	C	T				SILENT- NONCODING	kinase	Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa.	1.70E-234	
69	cg43957170	2179	AAAATTAGCCGG GCGTGGTGGCG CA[T/C]GCCCTGTA GTCCCAGCTACT CGGGAG	T	C				SILENT- NONCODING	kinase	Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa.	1.70E-234	

70	cg38438124	1767	ACTTTGTGTATA TGTGTGTGTGTG TIG/gapJTGTTGG GGGGGGGTGAG TGTGTGCG	G	gap				SILENT- NONCODING	kinase	Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KII- ALPHA) (1- PHOSPHATIDYLINOSITOL-4- PHOSPHATE KINASE) (PTDINS(4)P- 5-KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS MUSCULUS (MOUSE), 405 aa.	2.80E-216	10
71	cg38438124	1769	TTTGTGTATATG TGTGTGTGTGTG TIG/gapJTTGGGG GGGGGTGAGTG TGTGCGCG	G	gap				SILENT- NONCODING	kinase	Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KII- ALPHA) (1- PHOSPHATIDYLINOSITOL-4- PHOSPHATE KINASE) (PTDINS(4)P- 5-KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS MUSCULUS (MOUSE), 405 aa.	2.80E-216	10
72	cg42923882	123	AGTGGGCAGGG ACCCTGGGAGC CTC/C/AJATTCTC AATGCCCCACCC TTTACCT	C	A				SILENT- NONCODING	kinase	Human Gene SPTREMBL-ID:Q92961 MAP KINASE KINASE MEK5B - HOMO SAPIENS (HUMAN), 448 aa.	1.80E-196	
73	cg43948037	1031	AAAGTTCTCGAA ATGCTTCATCCC C/G/AJACAAAGC AAATTTCATGTC CGTCAG	G	A				SILENT- NONCODING	kinase	Human Gene SWISSPROT- ID:Q00532 SERINE/THREONINE- PROTEIN KINASE KKIALRE (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 358 aa.	6.10E-189	

74	cg43948037	1106	CTGTTGCTTTCC CTGGGGTGTC AG[G/A]CTCAC AGGGAGTCAG AATCTTCT	G	A				SILENT- NONCODING	kinase	Human Gene SWISSPROT- ID:Q00532 SERINE/THREONINE- PROTEIN KINASE KKIALRE (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 358 aa.	6.10E-189	
75	cg43948037	1115	TCCCTGGGGTGT CCAGGCTCAC AG[G/C]GGAGTC AGAATCTTCTGG TTCTCCC	G	C				SILENT- NONCODING	kinase	Human Gene SWISSPROT- ID:Q00532 SERINE/THREONINE- PROTEIN KINASE KKIALRE (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 358 aa.	6.10E-189	
76	cg43948037	1124	TGTCAGGCTCA CCAGGGGAGTC AG[A/G]ATCTTCT GGTTCTCCCTTT TCATCA	A	G				SILENT- NONCODING	kinase	Human Gene SWISSPROT- ID:Q00532 SERINE/THREONINE- PROTEIN KINASE KKIALRE (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 358 aa.	6.10E-189	
77	cg43948037	1134	CACCAAGGGAG TCAGAACTTCT GGT[C/T]CTCCCT TTTCATCAAGTC TTCTAA	T	C				SILENT- NONCODING	kinase	Human Gene SWISSPROT- ID:Q00532 SERINE/THREONINE- PROTEIN KINASE KKIALRE (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 358 aa.	6.10E-189	
78	cg42703622	2409	TGTGGGTTGACA GATTTTAAATA [G/C]AATTAGAG TATTGGGGTTT TGTT	G	C				SILENT- NONCODING	kinase	Human Gene SPTREMBL-ID:Q12792 PROTEIN TYROSINE KINASE - HOMO SAPIENS (HUMAN), 350 aa.	3.00E-187	12
79	cg43336176	5568	TGCTGCTGCTGC TGCTGCTGGG GG[G/gap]ATCAC AGACCATTTCTT TCITTCGG	G	gap				SILENT- NONCODING	kinase	Human Gene SPTREMBL-ID:Q16205 MYOTONIN PROTEIN KINASE - HOMO SAPIENS (HUMAN), 625 aa.	1.10E-164	19
80	cg43982923	610	ACGCAGGGGTC CCCGCGGCCGC CGC[G/A]ATGCA GAAATACGAGAA ACTGGAAA	G	A				SILENT- NONCODING	kinase	Human Gene SWISSPROT- ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.60E-159	19

81	cg43265203	688	ACATTCAAGCTC GGTGTGTTTCA C A C GCGTG GCCCCGGCTGC GGCGGTG	A	C				SILENT- NONCODING	kinase	Human Gene Homologous to SWISSNEW-ID:P54619 5'-AMP- ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA- 1 CHAIN) - HOMO SAPIENS (HUMAN), 331 aa. pcis:SWISSPROT- ID:P54619 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.	5.50E-124	
82	cg43966625	77	CGTGCCCGCG CGGGGACCACA ACC A C AAGTC GCGGCCGCCGC AGCCATGCG	A	C				SILENT- NONCODING	kinase	Human Gene Similar to SWISSPROT- ID:Q15119 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 2 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 2) - HOMO SAPIENS (HUMAN), 407 aa. pcis:SPTREMBL- ID:Q15119 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 407 aa.	3.20E-89	17
83	cg44004317	4772	CACCACGATGC GGACCCCACTG CCC G A GCTCG ACCTCCTCGG AGGGGGCGC	G	A				SILENT- NONCODING	kinasere ceptor	Human Gene SWISSNEW-ID:P04626 ERBB-2 RECEPTOR PROTEIN- TYROSINE KINASE PRECURSOR (EC 2.7.1.112) (P185ERBB2) (NEU PROTO-ONCOGENE) (C-ERBB-2) - HOMO SAPIENS (HUMAN), 1255 aa. pcis:SWISSPROT-ID:P04626 ERBB-2 RECEPTOR PROTEIN- TYROSINE KINASE PRECURSOR (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1255 aa.	0.00E+00	
84	cg43925424	300	TCGGCGCACAG TCGCTGCTCCG CGC G T CGCGC CCGGCGGCGCT CCAGGTGCT	G	T				SILENT- NONCODING	kinesin	Human Gene SWISSPROT- ID:Q07866 KINESIN LIGHT CHAIN (KLC) - HOMO SAPIENS (HUMAN), 569 aa.	1.90E-304	14

85	cg44002977	242	TAGAGGACACAG GGGTGCAGAGA GG[G/A]TGTCTT GAGGGTCCTTC CTAAGAGG	A				SILENT- NONCODING	kinesin	Human Gene Similar to SWISSPROT- ID:Q07866 KINESIN LIGHT CHAIN (KLC) - HOMO SAPIENS (HUMAN), 569 aa.	2.70E-60	6
86	cg27803682	2540	TTGAGCCTCCAG GCTTCTCCTTGA C[G/A]TCATTCTT CTCCTTCCTTGC TGCAA	A				SILENT- NONCODING	misc_cha nnel	Human Gene Similar to SPTREMBL- ID:P91197 SIMILAR TO LIGAND- GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	3.50E-81	
87	cg43971768	2349	GAAGTGCAGTCA A TGCACAGCTGG CG[A/G]CCAGCC AAAGGCATTTTA CTGAGCA	G				SILENT- NONCODING	nucl_rec pt	Human Gene SWISSNEW-ID:Q61324 ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2) - MUS MUSCULUS (MOUSE), 712 aa.	0.00E+00	15
88	cg43987181	1358	AAGCTTAGTACT T AAAAAGTCAAAA T[T/A]TTTTTGCA TGATAGAGGAGT GTAAA	A				SILENT- NONCODING	nucl_rec pt	Human Gene SWISSNEW-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS- TRANS ISOMERASE) (EC 5.2.1.8) (PIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR- ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa. pcis:SWISSPROT-ID:Q13451:51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS- TRANS ISOMERASE) (EC 5.2.1.8) (PIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR- ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa.	9.40E-248	6

89	cg43263644	143	GCCGGGACAGT GTTGTACAGTGT TTT/CJGGGCAT GCACGTGATACT CACACAG	T	C				SILENT- NONCODING	nucl_rec pt	Human Gene SWISSPROT- ID:Q03181 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR BETA (PPAR-BETA) (PPAR-DELTA) (NUCLEAR HORMONE RECEPTOR 1) (NUC1) (NUC1) - HOMO SAPIENS (HUMAN), 441 aa.	4.70E-237	6
90	cg44131079	3497	CGGTGATATTAC AAACAATGAAT TTC/TJGGAACATAT TATAGATTGGGC ACCTC	C	T				SILENT- NONCODING	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.pcds:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	0.00E+00	
91	cg44031914	153	GCACAGGGGAG TGAGGGCAGGG CGC/T/CJCGCAG GGGACACGCAG GGAGGGCCC	T	C				SILENT- NONCODING	oncogen e	Human Gene SWISSPROT- ID:Q01543 FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR) - HOMO SAPIENS (HUMAN), 452 aa.	4.70E-253	11 (11q24)
92	cg43932550	3136	CATCATAGAACT CCTTGTTGATCT C[G/A]TAGAGCT CAGGCACITTTGA AGAAGA	G	A				SILENT- NONCODING	oncogen e	Human Gene SPTREMBL-ID:Q13746 BCR-ABL MRNA OF ACUTE LYMPHOCTIC LEUKAEMIA (ALL) PATIENTS - HOMO SAPIENS (HUMAN), 386 aa.	2.30E-205 (22q11.2 1)	22 (22q11.2 1)
93	cg43932550	3312	GACAGGACCCA TTTTCTCATCTC CA[A/G]GCCCTTT TCCAAGTCCAGC TCACTC	A	G				SILENT- NONCODING	oncogen e	Human Gene SPTREMBL-ID:Q13746 BCR-ABL MRNA OF ACUTE LYMPHOCTIC LEUKAEMIA (ALL) PATIENTS - HOMO SAPIENS (HUMAN), 386 aa.	2.30E-205 (22q11.2 1)	22 (22q11.2 1)

94	cg43967268	598	ACGAGAGAAAGG AGCAGCTGAAA GTG[G/A]CCTGG ACTCCAGCCCTG GCTGTTGT	G	A				SILENT- NONCODING	oncogen e	Human Gene Similar to SWISSPROT- ID:P24407 RAS-RELATED PROTEIN RAB-8 (ONCOGENE C-MEL) - HOMO SAPIENS (HUMAN), AND CANIS FAMILIARIS (DOG), 207 aa.	1.90E-52	
95	cg43920534	1076	CGTCACTATGTA CTTGGTTTTGCG CT[<i>gap</i>]TTTTTTT CCTTAAAAAAA AAGGCC	T	gap				SILENT- NONCODING	phosphat ase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
96	cg43920534	763	CTTCATAAAACC AATCGAGAGAGA G[A <i>gap</i>]GGACTT AAATCCTGCTT ACCAAAA	A	gap				SILENT- NONCODING	phosphat ase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
97	cg43926887	1786	ATTGTTTTCAAC ATGAAGTAAAGA ATT/AACGTTGA GGCCTTTACTAT TAGCT	T	A				SILENT- NONCODING	phosphat ase	Human Gene SWISSPROT- ID:Q06190 PROTEIN PHOSPHATASE PP2A, 130 KD REGULATORY SUBUNIT (PR130) - HOMO SAPIENS (HUMAN), 1150 aa.	0.00E+00	3
98	cg43926887	1838	GTCTAATACTCC TGGGAGGAAGG AAIT/AJATATCTA TCTAGTAAGAAT TTTAAT	T	A				SILENT- NONCODING	phosphat ase	Human Gene SWISSPROT- ID:Q06190 PROTEIN PHOSPHATASE PP2A, 130 KD REGULATORY SUBUNIT (PR130) - HOMO SAPIENS (HUMAN), 1150 aa.	0.00E+00	3
99	cg43088901	2303	GAGCACGGTGT CAAGCTGCTCTG AG[C/T]CACAGT GGGATGAACCA GCCGGGGC	C	T				SILENT- NONCODING	phosphat ase	Human Gene SWISSNEW-ID:P30304 M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa.[<i>pcis</i> :SWISSPROT- ID:P30304 M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa.	4.00E-288	3 (3p21)

100	cg43920213	3664	GTGAGCCATAAT ATGATGGCCAG CA[G/gap]GTGGC GCTGCCCTCCAC CCATGGTG	G	gap				SILENT- NONCODING	phosphatase	Human Gene Similar to SWISSPROT- ID:P51452 DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE VHR) - HOMO SAPIENS (HUMAN), 185 aa.	6.00E-81	17
101	cg43969348	648	TGGGGGAAATG GGCCTCTTGGG GGT[C/gap]TCAC TGCACGGCTTGT TCATTGGCA	C	gap				SILENT- NONCODING	polymerase	Human Gene Similar to SPTREMBL- ID:Q15370 RNA POLYMERASE II TRANSCRIPTION FACTOR SIII P18 SUBUNIT - HOMO SAPIENS (HUMAN), 118 aa.	3.90E-59	16
102	cg43966692	331	TACGAATTGGCA TATTTGTTTATTT C/gap]TCAGTTTG TGAAAATGTCCT TAATT	C	gap				SILENT- NONCODING	polymerase	Human Gene Similar to SPTREMBL- ID:Q15369 RNA POLYMERASE II ELONGATION FACTOR SIII, P15 SUBUNIT - HOMO SAPIENS (HUMAN), 112 aa.	4.00E-57	8
103	cg43265754	4375	CGAGACCAAGCC TGGCCAACATG GTG[A/C]AACCC CATCTCTACTAA AAATACAA	A	C				SILENT- NONCODING	potassium channel	Human Gene SWISSPROT- ID:P48544 G PROTEIN-ACTIVATED INWARD RECTIFIER POTASSIUM CHANNEL 4 (GIRK4) (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 5) (HEART KATP CHANNEL) (KATP-1) (CARDIAC INWARD RECTIFIER) (CIR) (KIR3.4) - HOMO SAPIENS (HUMAN), 419 aa.	6.70E-185	
104	cg43265754	4389	CCAACATGGTGA AACCCCATCTCT A[C/T]TAAAAATA CAAAAATTAGCC GGGCG	C	T				SILENT- NONCODING	potassium channel	Human Gene SWISSPROT- ID:P48544 G PROTEIN-ACTIVATED INWARD RECTIFIER POTASSIUM CHANNEL 4 (GIRK4) (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 5) (HEART KATP CHANNEL) (KATP-1) (CARDIAC INWARD RECTIFIER) (CIR) (KIR3.4) - HOMO SAPIENS (HUMAN), 419 aa.	6.70E-185	

105	cg43922227	538	ATGTTGTGTTGG GTCCCCAGATTG C/C/TATTTGATT TTCTTGATCAT TTTCT	C	T				SILENT- NONCODING	reductase	Human Gene Homologous to SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.70E-150	14
106	cg43927549	1020	GTAAGCAGCACAG CTAGGAGGCC AG[G/gap]CGCAG GCAAAGAGAAAG ATGGTGCTG	G	gap				SILENT- NONCODING	reductase	Human Gene Homologous to SWISSPROT-ID:P16083 NAD(P)H DEHYDROGENASE (QUINONE) 2 (EC 1.6.99.2) (QUINONE REDUCTASE) (DT-DIAPHORASE) (AZOREDUCTASE) (PHYLLQUINONE REDUCTASE) (MENADIOLONE REDUCTASE) - HOMO SAPIENS (HUMAN), 231 aa.	1.60E-124	6 (6pter)
107	cg43957486	4041	TGTATCATAGAA ATGTAACTTTTG T/A/GIAGACAAA GGTTTTCCTCTT CTATTT	A	G				SILENT- NONCODING	struct	Human Gene SWISSPROT- ID:P07204 THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN) - HOMO SAPIENS (HUMAN), 575 aa.	0.00E+00	20 (20p11.2)
108	cg43973080	779	GACACTAGGAAT TCTTAAAAAGA A/A/gap]GATGTT GGAAGCAGAAC ACTTACTA	A	gap				SILENT- NONCODING	struct	Human Gene TREMBLNEW- ID:G2304981 MYOSIN VI - HOMO SAPIENS (HUMAN), 1262 aa.	0.00E+00	6
109	cg42914441	2306	CTCTGACCTGAG TCTTTGTTTTAAG [A/GIAGTATTTGT CTTCCTTTGTCT AATG	A	G				SILENT- NONCODING	struct	Human Gene Homologous to SWISSPROT-ID:P26044 RADIXIN (MOESIN B) - SUS SCROFA (PIG), 583 aa.	5.40E-133	22 (22q12.2)
110	cg43942318	1006	GGACACCCCTCG GACCCTCGAAAA CG[C/T]CTCAGG AGCTATGAAGAC ATGATTG	C	T				SILENT- NONCODING	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	4.80E-123	11

111	cg43929933	431	CAGGCCAGGCC TGTTGTCTCCACC TG[C/G]ACAGGC ATTCTCCTTGTT CCAGAAA	C	G				SILENT- NONCODING	struct	Human Gene Homologous to SPTREMBL-ID:P97756 CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE IV KINASE ISOFORM - RATTUS NORVEGICUS (RAT), 505 aa.	1.80E-117	12
112	cg43929933	541	CGCAGCCCAA GTGTCAACAAGG GG[C/T]TCAATAA GGCTTCTGGGA GCCACT	C	T				SILENT- NONCODING	struct	Human Gene Homologous to SPTREMBL-ID:P97756 CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE IV KINASE ISOFORM - RATTUS NORVEGICUS (RAT), 505 aa.	1.80E-117	12
113	cg43929933	590	CTGGCAGCTGG TGGGATGGAAG GGG[G/gap]AGGT GGAAAAGGGCA GAGGAAATGG	G	gap				SILENT- NONCODING	struct	Human Gene Homologous to SPTREMBL-ID:P97756 CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE IV KINASE ISOFORM - RATTUS NORVEGICUS (RAT), 505 aa.	1.80E-117	12
114	cg43070037	7268	AGGTCAGGAGTT TGAGACCCAGCCT A[G/A]CCCAACAT GGTGAAACCCC ATCTCTA	G	A				SILENT- NONCODING	synthase	Human Gene SWISSPROT- ID:P35421 PHOSPHORIBOSYLFORMYLGLYCIN AMIDINE SYNTHASE (EC 6.3.5.3) (FGAM SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT) (ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1354 aa.	0.00E+00	

115	cg43070037	7269	GGTCAGGAGTTT GAGACGAGCCT AG[C/G]CAACAT GGTGAACCC ATCTCTAC	C	G				SILENT- NONCODING	synthase	Human Gene SWISSPROT- ID:P35421 PHOSPHORIBOSYLFORMYLGLYCIN AMIDINE SYNTHASE (EC 6.3.5.3) (FGAM SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT) (ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1354 aa.	0.00E+00	
116	cg43070037	7352	GTGGGTGCCTG TAATCCCAGCTA CTC/TJGGGAGG CTGAGGCAGGA GAATCACC	C	T				SILENT- NONCODING	synthase	Human Gene SWISSPROT- ID:P35421 PHOSPHORIBOSYLFORMYLGLYCIN AMIDINE SYNTHASE (EC 6.3.5.3) (FGAM SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT) (ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1354 aa.	0.00E+00	
117	cg43070037	7365	ATCCGAGCTACT CGGGAGGCTGA GG[C/T]AGGAGA ATCACCTGAACC TAGGAGG	C	T				SILENT- NONCODING	synthase	Human Gene SWISSPROT- ID:P35421 PHOSPHORIBOSYLFORMYLGLYCIN AMIDINE SYNTHASE (EC 6.3.5.3) (FGAM SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT) (ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1354 aa.	0.00E+00	

118	cg43070037	7366	TCCAGCTACTC GGGAGGCTGAG GC[A/G]GGAGAA TCACCTGAACCT AGGAGGC	A	G				SILENT- NONCODING	synthase	Human Gene SWISSPROT- ID:P35421 PHOSPHORIBOSYLFORMYLGLYCIN AMIDINE SYNTHASE (EC 6.3.5.3) (FGAM SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT) (ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1354 aa.	0.00E+00	
119	cg43123664	240	AGTACGCCAGC CCGGGGCGGCC CCG[A/C]ATGTA CATGTTCCACGC GGGATTCC	A	C				SILENT- NONCODING	synthase	Human Gene Similar to SWISSPROT- ID:O35696 ALPHA-2,8- SIALYLTRANSFERASE (EC 2.4.99.-) (ST8SIAII) (SIALYLTRANSFERASE X) (STX) (POLYSIALIC ACID SYNTHASE) - MUS MUSCULUS (MOUSE), 375 aa.	3.10E-59	18
120	cg21428405	17	NACGCGTTGGC GTCGTT/CJCTC GTTGAGCTCATC AATCCACCAC	T	C				SILENT- NONCODING	synthase	Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCIN AMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa.	2.20E-56	
121	cg43982633	811	ACACAGCCCCA GTTTGCTTTACA GC[C/G]CAAGTT ACAAACTGTCCC TTTAAAA	C	G				SILENT- NONCODING	tgfrecept or	Human Gene SWISSPROT- ID:P56159 GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF- BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1) - HOMO SAPIENS (HUMAN), 464 aa.	1.50E-254	
122	cg43054268	312	TCTAGATATTTAA CTGACCCACTAT [A/gap]TTCCTCA AGGATACTGCAT TTGGAC	A	gap				SILENT- NONCODING	thioester ase	Human Gene Similar to TREMBLNEW- ID:E307161 MITOCHONDRIAL VERY- LONG-CHAIN ACYL-COA THIOESTERASE - RATTUS NORVEGICUS (RAT), 453 aa.	3.50E-83	9

123	cg43054268	448	GACTATATGATC AAAGCCTTATAG C[A/gap]AAAAA ATTTTAAATATT TGCAA	A					SILENT- NONCODING	thioester ase	Human Gene Similar to TREMBLNEW- ID:E307161 MITOCHONDRIAL VERY- LONG-CHAIN ACYL-COA THIOESTERASE - RATTUS NORVEGICUS (RAT), 453 aa.	3.50E-83	9
124	cg43943775	259	TGAAGATTACCC CCACACCTGTGT G[A/G]CAAGTGA TCAAAAAGGAAC AGGACC	A	G				SILENT- NONCODING	tm7	Human Gene SWISSPROT- ID:P21554 CANNABINOID RECEPTOR 1 (CB1) (CB-R) (CANN6) HOMO SAPIENS (HUMAN), 472 aa.	5.40E-252	6 (6q14)
125	cg42886565	3473	GGCAACAAAAG CGAAACTCCATC TC[A/gap]AAAAA AAAGAGCTATAG GATCTTTA	A	gap				SILENT- NONCODING	tm7	Human Gene SWISSPROT- ID:P25116 THROMBIN RECEPTOR PRECURSOR - HOMO SAPIENS (HUMAN), 425 aa.	4.40E-225	5 (5q13)
126	cg42886565	3481	AAGCGAAACTCC ATCTCAAAAAA A[A/gap]GAGCTA TAGGATCTTTAC AATATAT	A	gap				SILENT- NONCODING	tm7	Human Gene SWISSPROT- ID:P25116 THROMBIN RECEPTOR PRECURSOR - HOMO SAPIENS (HUMAN), 425 aa.	4.40E-225	5 (5q13)
127	cg42886565	4462	TCCTCTGTCTGC TGGCTGGCCGC GT[G/A]TATGAAG AAGACTAATTGG ACACAG	G	A				SILENT- NONCODING	tm7	Human Gene SWISSPROT- ID:P25116 THROMBIN RECEPTOR PRECURSOR - HOMO SAPIENS (HUMAN), 425 aa.	4.40E-225	5 (5q13)
128	cg42886565	4483	GCGTGTATGAAG AAGACTAATTGG A[C/T]ACAGAGC CGTGATGAATTA AAGTCT	C	T				SILENT- NONCODING	tm7	Human Gene SWISSPROT- ID:P25116 THROMBIN RECEPTOR PRECURSOR - HOMO SAPIENS (HUMAN), 425 aa.	4.40E-225	5 (5q13)
129	cg43307001	1796	GCCTCCCGGGT TCAAGTGATTCT CCIT/CIGCCTCA GCCTCCCAAGTA GCTGGGAT	T	C				SILENT- NONCODING	tm7	Human Gene SWISSPROT- ID:P35348 ALPHA-1A ADRENERGIC RECEPTOR (ALPHA 1A- ADRENOCEPTOR) (ALPHA-1C ADRENERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 466 aa.	2.50E-199	

130	cg43307001	1898	GGGGTTTCAACAG TGTTGGCCAGG CTG/AGTCTCG AACTCCTGACCT CAAGTGA	G	A			SILENT- NONCODING	tm7	Human Gene SWISSPROT- ID:P35348 ALPHA-1A ADRENERGIC RECEPTOR (ALPHA 1A- ADRENOCEPTOR) (ALPHA-1C ADRENERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 466 aa.	2.50E-199	
131	cg43307001	1909	ATGTTGGCCAG GCTGGTCTCGAA CTC/TCTGACCT CAAGTGATCCGC CCACCT	C	T			SILENT- NONCODING	tm7	Human Gene SWISSPROT- ID:P35348 ALPHA-1A ADRENERGIC RECEPTOR (ALPHA 1A- ADRENOCEPTOR) (ALPHA-1C ADRENERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 466 aa.	2.50E-199	
132	cg43047341	2113	GGTGGATCACCT GAGGTCACGAG TTTC/TGAGACCA GCCTGACCAACA TGGAGA	C	T			SILENT- NONCODING	tm7	Human Gene SWISSPROT- ID:P21731 THROMBOXANE A2 RECEPTOR (TXA2-R) (PROSTANOID TP RECEPTOR) - HOMO SAPIENS (HUMAN), 369 aa.	2.80E-190	
133	cg43965652	891	TCCATTTCTTTT CTTTTTTTTTTT /gap]TAAGTGAGA CTACATTGGCAA ATGG	T	gap			SILENT- NONCODING	tnf	Human Gene Homologous to SPTREMBL-ID:Q99732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa.	4.50E-121	16
134	cg43965652	892	CCATTTCTTTTCT TTTTTTTTTTTTT gap]AAGTGAGAC TACATTGGCAAA TGGG	T	gap			SILENT- NONCODING	tnf	Human Gene Homologous to SPTREMBL-ID:Q99732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa.	4.50E-121	16
135	cg43965652	412	TTCCAAACATCA AATGAAGGGG ATC/gap]AATGG TTACCACTATCG TTTTCAAC	C	gap			SILENT- NONCODING	tnf	Human Gene Homologous to SPTREMBL-ID:Q99732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa.	4.50E-121	16

136	cg43985709	933	AGCTCACTTTGG CCCTTCTCCACC CIA/GITCCCAAC CCCATTGCTAAC AACATG	A	G				SILENT- NONCODING	tnf	Human Gene Similar to SWISSPROT- ID:Q13829 TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN) - HOMO SAPIENS (HUMAN), 316 aa.	1.70E-51	16
137	cg44027791	1118	GCCACAGGGCT CCTTCCACCAG GG[G/gap]CCCA GGGAGGACACA GGTGGGGGAC	G	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT- ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	17
138	cg44027791	1173	TCCTCAGGGCCT CCGCGCGCAGT TG[G/A]CCTTACA AGTCTTCGTGA CCAGGT	G	A				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT- ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	17
139	cg44027791	916	AAGGGTCCCAC GCGTCCTGGTTT A[G/A]AACGTCTC ATTGGGCACGG CCAGTG	G	A				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT- ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	17
140	cg44027791	930	GTCCTGGTTTAG AACGTCTCATTG G[G/gap]CACGG CCAGTGTCCACA GTCTGGGC	G	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT- ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	17
141	cg43984418	923	TATGCAATGTTT AGCATTTTTTTT [T/gap]TCACAGC ACTAGAGACCCCT GTAAA	T	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT- ID:P23771 TRANS-ACTING T-CELL SPECIFIC TRANSCRIPTION FACTOR GATA-3 - HOMO SAPIENS (HUMAN), 443 aa.	2.40E-255	10 (10p15)
142	cg43984418	937	CATTTTTTTTTT CACAGCACTAGA [G/A]ACCCGTGTTA AATAGGGGATAT GAGT	G	A				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT- ID:P23771 TRANS-ACTING T-CELL SPECIFIC TRANSCRIPTION FACTOR GATA-3 - HOMO SAPIENS (HUMAN), 443 aa.	2.40E-255	10 (10p15)

143	cg43945210	543	CAGACAGACACA AGGTTCTTTTTT T/gap]GTTTGT TGTTTTCTCTCG CCAAC	T	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT- ID:Q60632 COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF1) - MUS MUSCULUS (MOUSE), 422 aa.	6.40E-235	5
144	cg43917396	915	TAGGGGCTGAA ACGCAGTCGGG GCC[G/gap]GGC ACTGCCCAGGA AGGGACTCCGG	G	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	6.90E-68	
145	cg43949162	510	TAGACAATACCA TCTCTAGGAACA C[A/G]CTGTCACT CACACATGGATG TGTTG	A	G				SILENT- NONCODING	transfere se	Human Gene Homologous to TREMBLNEW-ID:G2738933 GLUTATHIONE TRANSFERASE (EC 2.5.1.18) - HOMO SAPIENS (HUMAN), 222 aa.	1.30E-115	6
146	cg41653463	2407	TGTGCGTGCGT GTGTGTGTGT GT[gap]TGTAT CGTGTGTGTGT TTTTGTTT	G	gap				SILENT- NONCODING	transport	Human Gene SWISSPROT- ID:P31641 SODIUM- AND CHLORIDE- DEPENDENT TAURINE TRANSPORTER - HOMO SAPIENS (HUMAN), 620 aa.	0.00E+00	3 (3p25)
147	cg41653463	2408	GTGCGTGCGTG TGTTGTGTGTGT TG[T/gap]GTATC GTGTGTGTGTGT TTTTGTTT	T	gap				SILENT- NONCODING	transport	Human Gene SWISSPROT- ID:P31641 SODIUM- AND CHLORIDE- DEPENDENT TAURINE TRANSPORTER - HOMO SAPIENS (HUMAN), 620 aa.	0.00E+00	3 (3p25)
148	cg43285429	388	CCCAGTCAAGAT AAGGAGGATCC CA[G/A]CAGCTC CCCTCCGAGGTT GGGCTCT	G	A				SILENT- NONCODING	transport	Human Gene SWISSNEW-ID:P02730 BAND 3 ANION TRANSPORT PROTEIN (ANION EXCHANGE PROTEIN 1) (AE 1) - HOMO SAPIENS (HUMAN), 911 aa. pdis:SWISSPROT-ID:P02730 BAND 3 ANION TRANSPORT PROTEIN (ANION EXCHANGE PROTEIN 1) (AE 1) - HOMO SAPIENS (HUMAN), 911 aa.	0.00E+00	17 (17q21)

149	cg43918636	3322	AGCAGCAGCTG TTGGAGTAGAAC CG[C/A]GTCCAG GGCGCGACCAT CTTCATCG	C	A				SILENT- NONCODING	transport	Human Gene Similar to SWISSPROT- ID:Q15012 GOLGI 4- TRANSMEMBRANE SPANNING TRANSPORTER MTP (KIAA0108) - HOMO SAPIENS (HUMAN), 233 aa.	5.40E-52	
150	cg44005525	721	TAAGCAGCTCTC TTCTGTGACAGA C[A/gap]AATCAT GTAAGAACTGTG AAACCCC	A	gap				SILENT- NONCODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
151	cg44005525	743	GACAAATCATGT AAGAACTGTGAA A[C/A]CCCCAGTTT ATGTAGCGTATC TCTTG	C	A				SILENT- NONCODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
152	cg40986905	3075	ATTTTATAGTAG GACGGGGTTTC AC[C/T]GTGTTAG CCAGGATGGTCT CGATCT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14162 KIAA0149 PROTEIN - HOMO SAPIENS (HUMAN), 830 aa.	0.00E+00	
153	cg43303871	1999	AATAAGGGAGAA CTACTATTTTTT [gap/T]AAGATCT CAAAATAATTAA TAATAA	gap	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25444 KIAA0518 PROTEIN - HOMO SAPIENS (HUMAN), 650 aa (fragment).	0.00E+00	
154	cg43303871	1999	AATAAGGGAGAA CTACTATTTTTT [gap/T]AAGATCT CAAAATAATTAA TAATAA	gap	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25444 KIAA0518 PROTEIN - HOMO SAPIENS (HUMAN), 650 aa (fragment).	0.00E+00	

155	cg43918386	3972	CTTCTACCCCAT GGGTAAATGTAT TTT/CJACATATTA CCAAGAGAAGAA GCACA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SP TREMBL- ACC:Q14511 ENHANCER OF FILAMENTATION 1 - HOMO SAPIENS (HUMAN), 834 aa.	0.00E+00	6
156	cg43923712	501	AGGAATCCTGGA CAGGAGTTTCT G/C/TJAGAGCG TTTAAACCCTA CCGAAT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SP TREMBL- ACC:Q12996 CLEAVAGE STIMULATION FACTOR 77KDA SUBUNIT - HOMO SAPIENS (HUMAN), 717 aa.	0.00E+00	11
157	cg43936083	189	GCTAACTGGTGA A CAGTTATAAAAA C/A/G/C/AAAAAG GAGCCTGGGAA ACAGCAA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SP TREMBL- ACC:O15089 KIAA0385 - HOMO SAPIENS (HUMAN), 1370 aa.	0.00E+00	
158	cg43936393	382	AAAAACAAGTTT A CAGTAAAAAAA A/A/gap/JACTAAA ACAAACACTGAA GTAGAGT	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD22032 THYROID HORMONE RECEPTOR- ASSOCIATED PROTEIN COMPLEX COMPONENT TRAP240 - HOMO SAPIENS (HUMAN), 2174 aa.	0.00E+00	17
159	cg43936393	383	AAACAAAGTTTC A AGTAAAAAAA A/A/gap/JCTAAAA CAACACTGAAG TAGAGTT	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD22032 THYROID HORMONE RECEPTOR- ASSOCIATED PROTEIN COMPLEX COMPONENT TRAP240 - HOMO SAPIENS (HUMAN), 2174 aa.	0.00E+00	17
160	cg43940465	304	ACTGTATTATTGA G TTTACATGGGCTT G/A/JAAAGCAAAG AAAAATGAGTCC CTTC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SP TREMBL- ACC:O60300 KIAA0553 PROTEIN - HOMO SAPIENS (HUMAN), 1095 aa (fragment).	0.00E+00	

161	cg43940880	10186	TAGTTGTGAAGA ACTGTACAAAA A[AGAP]JGCTTC TGGAGATTCTT TGGCAGA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P53794 SODIUM/MYO- INOSITOL COTRANSPORTER (NA(+)/MYO-INOSITOL COTRANSPORTER) - Homo sapiens (Human), 718 aa.	0.00E+00	21
162	cg43950657	1956	TTGGGATCCTG ATCAATCTTTCT [G/A]ATGTTGTTG AAATGACAAAG TTGG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q13009 T-LYMPHOMA INVASION AND METASTASIS INDUCING PROTEIN 1 (TIAM1 PROTEIN) - Homo sapiens (Human), 1591 aa.	0.00E+00	21 (21q22.1)
163	cg43950657	2033	CAGCTGCCAAAA CCGTGTGTGCAA G[A/G]GCGCGAC CTAAGGGGACAT TCTTGT	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q13009 T-LYMPHOMA INVASION AND METASTASIS INDUCING PROTEIN 1 (TIAM1 PROTEIN) - Homo sapiens (Human), 1591 aa.	0.00E+00	21 (21q22.1)
164	cg43973740	485	TGAAGCAAAACA ACAAACAAAAA A[AGAP]GGAGAG CTTCATTAGTAG CCAAGAT	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q61123 MATERNAL EMBRYONIC MESSAGE 3 (MEM3) - MUS MUSCULUS (MOUSE), 754 aa.	0.00E+00	16 (12q12)
165	cg43980521	1011	GGCATGGGTC CCTCCAGGAAG GCTT[G]GGTTA GAGTCCCAGGG TGGTCCCCA	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA20795 KIAA0337 PROTEIN - HOMO SAPIENS (HUMAN), 1510 aa.	0.00E+00	11
166	cg43980521	551	CCCTCAGCTTTG GGGGGTCTTC CTG[A]AAGGGG CTTCCCTTGGCA GAAGGGG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA20795 KIAA0337 PROTEIN - HOMO SAPIENS (HUMAN), 1510 aa.	0.00E+00	11
167	cg43980521	873	AGCATCTTGATC TAGAGGACTGA GG[G/A]CAGCCC CATCAGGCTGG GGCCCTGG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA20795 KIAA0337 PROTEIN - HOMO SAPIENS (HUMAN), 1510 aa.	0	11

168	cg44019839	3287	AGCTACACAGAGT GAAATAACTTAG GTT/CIACTTTCTG TTTTTTTAAAAA AATA	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q99743 NEURONAL PAS DOMAIN PROTEIN 2 (NEURONAL PAS2) (MEMBER OF PAS PROTEIN 4) (MOP4) - Homo sapiens (Human), 824 aa.	0	
169	cg44021891	787	AGAAGACCTGG CTTCCTTACAAC AGG/AJGACAGG CTGGTGGCTGG GGCTAGAG	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q92560 BRCA1 ASSOCIATED PROTEIN 1 (MYELOBLAST KIAA0272) - HOMO SAPIENS (HUMAN), 729 aa.	0	3
170	cg44021891	869	GCCCCCAGCTA GGACCCCTGTAGT TGGAJGACCGT GGCATGATACAA GGACCTG	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q92560 BRCA1 ASSOCIATED PROTEIN 1 (MYELOBLAST KIAA0272) - HOMO SAPIENS (HUMAN), 729 aa.	0	3
171	cg44921773	2876	TTCTGAGACAGG GTCTTGCTCTGT C[G/A]CCCAGGC TGGAGTGCAATG GCACGA	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13471 REPLICATION CONTROL PROTEIN 1 - HOMO SAPIENS (HUMAN), 861 aa.	0	1
172	cg44921773	2955	GGGCTCAAGTG ATCCTCCCACCT CA[A/G]CCTCCC GAGTAGCTGAG ACTACAGG	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13471 REPLICATION CONTROL PROTEIN 1 - HOMO SAPIENS (HUMAN), 861 aa.	0	1
173	cg43961485	650	GGTCTCCTCAGT GGTCTATTTTAG GTT/GJGTGGTTTT TTTTTTTTTTTT ACTG	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O60398 TXBP151 - HOMO SAPIENS (HUMAN), 563 aa.	1.5E-303	7
174	cg43985955	2111	GAGCACAGATAC AGTTTATGTAAC TTT/AJGATGGAAG AAAATGGAATTA CTCCA	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	2.7E-299	

175	cg44916647	1142	GCTCAGCAGCC CCTAGGAAGTTA AGC/TTGAGAGC TACAGGGCAGG GGGGCTCC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75057 KIAA0469 PROTEIN - HOMO SAPIENS (HUMAN), 539 aa.	4.3E-299	1
176	cg44916647	494	TCTGTACATGTA ACATGTGGCCAT G[C]gap]CCAGGC ATCCAGCATCT ATCCTGA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75057 KIAA0469 PROTEIN - HOMO SAPIENS (HUMAN), 539 aa.	4.3E-299	1
177	cg44021459	2082	GGTCACTGTTTC CTCGGCATCGT GC/T/CjGCCTGG AGAGAACTCCC GACCGGGA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC16046 FIP2 - HOMO SAPIENS (HUMAN), 577 aa.	1E-297	
178	cg43926814	372	TAGAAATTTCTAT CCCCCCCCATTT [C/T]TCCAGTAAT AAAAAGTAGTGC TGGG	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q13573 NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) (NUCLEAR RECEPTOR COACTIVATOR NCOA- 62) - Homo sapiens (Human), 536 aa.	5E-289	14
179	cg43926814	412	GTAGTGCTGGG ATCTGGCACCCCA GA/T/CjTTGGTTT TTATCCTGACCA TTTACA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q13573 NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) (NUCLEAR RECEPTOR COACTIVATOR NCOA- 62) - Homo sapiens (Human), 536 aa.	5E-289	14
180	cg43931431	1415	AGCCATGTACGT GAAATTGCTTGG GATACCTGAAC TCCCGCTGGAAT TTCTA	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q14154 HYPOTHETICAL PROTEIN KIAA0141 - Homo sapiens (Human), 515 aa.	7.2E-281	5
181	cg44031765	277	ATGCACCTGGC CCACATGGCTG GGC[G/A]CTGCA GCCTGCACTCCA CTTCCAGG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14776 LZTR-1 - HOMO SAPIENS (HUMAN), 552 aa.	4.6E-279	22

182	cg44031765	4030	CATCTTTATAGG CCACCACTGTGT G[C/T]TTGCTGC GCCGGGCACCC ACGAACT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14776 LZTR-1 - HOMO SAPIENS (HUMAN), 552 aa.	4.6E-279	22
183	cg43970492	331	TGCTTTGTGCT TCAAGATGCATG C[A/C]CATCCTG GCTTAGTGTC AAGTAT	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:P78395 PREFERENTIALLY EXPRESSED ANTIGEN OF MELANOMA - HOMO SAPIENS (HUMAN), 509 aa.	3.60E-270	22
184	cg42847874	1118	ACAAAAATTAGC CGGGCATGGTG GC[G/A]CACGCC TGAGTCCCAGC TACTTAG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA34492 KIAA0772 PROTEIN - HOMO SAPIENS (HUMAN), 468 aa.	6.30E-258	20
185	cg43951020	534	GAGTGCAGTGG CTCACTGCAACC TC[C/T]GCCCTCC CAGGTTCAAGCA ATTCTCC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O76021 PBK1 PROTEIN - HOMO SAPIENS (HUMAN), 516 aa.	6.60E-255	
186	cg43951020	552	CAACCTCCGCCT CCCAGGTTCAAG C[A/G]ATTCTCCT GCCTCAGCCTC CCTAGT	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O76021 PBK1 PROTEIN - HOMO SAPIENS (HUMAN), 516 aa.	6.60E-255	
187	cg43971614	2720	ACCATTGCTTTG GTCAATTCAACC T[G/A]GGGGGAA AAGAGTCAAATA TGTCCTA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13283 GAP SH3 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 466 aa.	5.30E-253	5
188	cg43971614	2802	CTCTGCACCACA GCACCGAGGAT AGT[C]ACAAACC CCTCACGCGTCT GCGTCC	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13283 GAP SH3 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 466 aa.	5.30E-253	5

189	cg43962954	192	CGGGCTCCCA TGCAGCCCTAGA GA[C/gap]GGGA GAAGTCCAGTGT GCTGTTCCA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75455 HERPESVIRUS ENTRY PROTEIN B - HOMO SAPIENS (HUMAN), 479 aa.	4.80E-252	19
190	cg43917689	1684	AGGCAACACCT GTGGAGGAAGG GCA[C/T]TGGGGC AAAAGCTCACCT CAGAAAGTG	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q92551 MYELOBLAST KIAA0263 - HOMO SAPIENS (HUMAN), 441 aa.	3.50E-240	3
191	cg43917685	2176	TCAGATGACTTT ACAACCAAGGG AGIT/CJACACAG GGCAACAACAAA TTAGAGG	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC97961 S164 - HOMO SAPIENS (HUMAN), 735 aa (fragment).	2.50E-230	14
192	cg43287642	307	GCAACTATTTT AAAACCCAAAGG A[G/A]AAAGGAT GGTACTACCATA AATCAC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD20347 NEBULIN - HOMO SAPIENS (HUMAN), 977 aa (fragment).	3.50E-224	
193	cg43986954	1072	AGTGGAAACATT TTTGTTCAATTTC IT/CJAGGAATTT CTCTTGGGAAA GTCG	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC68871 METHYL-CPG BINDING PROTEIN MBD2 - HOMO SAPIENS (HUMAN), 411 aa.	9.40E-224	18
194	cg42882543	3078	TCCCGAGTAGCT GGGATTACAGG CAIT/CJGCGCCA CCACGCCGAGC TAATTTT	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75177 KIAA0693 PROTEIN - HOMO SAPIENS (HUMAN), 404 aa (fragment).	2.30E-220	
195	cg43062833	1567	TGAAAAGTATTA TGGAAATCACTG CIAITGACACAG AAAAGTAATTCA GATGTT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q93088 BETAINE-- HOMOCYSTEINE S- METHYLTRANSFERASE (EC 2.1.1.5) - Homo sapiens (Human), 406 aa.	2.10E-219	5

196	cg43959148	342	AGACTAGTGTGG GCCTTGGCCC CC[C/gap]TCATT TTGACATCCTTC CAGATGGT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75955 FLOTILLIN-1 - HOMO SAPIENS (HUMAN), 427 aa.	1.40E-215	6
197	cg43950766	385	GTTACACATTTAG TGAACCTGCATT T[C/gap]ATGGGG GGGGGGGGGT ACACAGTA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD4491 PTD004 - HOMO SAPIENS (HUMAN), 396 aa.	5.30E-214	22
198	cg43958860	1340	TCTGTCTTTTATT TAACAAAAAATG[T/C]AATTAACTG TAAACTTGAAT CAAG	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P48745 NOV PROTEIN HOMOLOG PRECURSOR (NOVH) - Homo sapiens (Human), 357 aa.	6.00E-206	8 (8q24.1)
199	cg43968205	1516	CTATAGCAGAGG GGTTATGGGG GC[G/A]GGAGGG TAGACTGACATA CAGAAAGT	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB46373 HYPOTHETICAL 71.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 653 aa (fragment).	6.90E-206	
200	cg43950996	825	ACGCCAGTCCA GAAAGAAAGTG CTG[G/A]AGCCC CTGCTCTGTCT CTCCATCA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.20E-204	1
201	cg44924222	1787	TAAGGGTGAGC AGCAGCAGGAG CGC[A/T]TTGAAG AAGAAGTAGAAG GGGATGT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:P27539 EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1) - Homo sapiens (Human), 372 aa.	2.7E-203	
202	cg44924222	1834	ATGTCAGGCACC GTGCGCAGACT GC[A/G]GTGACT GGTGGCATACA GGACCTTG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:P27539 EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1) - Homo sapiens (Human), 372 aa.	2.7E-203	

203	cg44924222	2073	GTACCGGAAGG CGTAGGAGGAG ACG A/G TGAGG ATGAGAGTGACC ACGTGGTG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:P27539 EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1) - Homo sapiens (Human), 372 aa.	2.7E-203	
204	cg44916575	1943	GAGGACAAAAAC AGAAAGCCCTGT G A/T GTGTGGG AAACTCCGCTG CAGAGA	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q16842 BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE (EC 2.4.99.4) (CMP-N- ACETYLNEURAMINATE-BETA- GALACTOSAMIDE-ALPHA-2,3- SIALYL- TRANSFERASE) - HOMO SAPIENS (HUMAN), 350 aa.	3.7E-197	
205	cg42650960	2321	GGCTGGAGTGC AGTGGCACGAT CTC G A GCTCA CTGCAAGCCTCC GCCTCCCG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q10981 GALACTOSIDE 2-L- FUCOSYLTRANSFERASE 2 (EC 2.4.1.69) (GDP-L-FUCOSE:BETA- D- GALACTOSIDE 2-ALPHA-L- FUCOSYLTRANSFERASE 2) (ALPHA(1,2)FT 2) (FUCOSYLTRANSFERASE 2) (SECRETOR BLOOD GROUP ALPHA- 2- FUCOSYLTRANSFERASE) (SECRETOR FACTOR) (SE) (SE2) - Homo sapiens (Human), 343 aa.	2E-189	
206	cg43947129	2163	CTGGGGGCGTC CATGGTGCGGC GGC G C AGGGC GGTGAGTCAGC CAAGGAGGA	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P10658 PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP) - Oryctolagus cuniculus (Rabbit), 370 aa.	3E-188	
207	cg43922383	199	ATCTGAAAATGG TGTGTGGCGTC GC G A CGCGCC AGCTATCGTCAG TGCCTTT	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa.	7.3E-185	2

208	cg43922383	222	CGCGCGCCAGC TATCGTCAGTGC CT[gap]GJTATT GCCATTGGGTTT GTGACTGT	gap	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa.	7.3E-185	2
209	cg43922383	239	TCAGTGCCTTTA TTGCCATTGGGT TIT[gap]GTGACT GTTGATATAGTG ACGACCT	T gap	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa.	7.3E-185	2
210	cg43922383	250	ATTGCCATTGGG TTTGTGACTGTT GIA/GJTATAGTA CGACCTCAGGA GCAACA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa.	7.3E-185	2
211	cg43922383	263	TTGTGACTGTTG ATATAGTGACGA CIC/GJTCAGGAG CAACAGGTGGG TTAAAA	C	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa.	7.3E-185	2
212	cg43953935	458	CTTTTAAATAAA TGACTGCGAGT GIA/GJGTGTAAT TCTGAGAAAATT ACATT	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD41634 LYOSOMAL TRAFFICKING REGULATOR 2 - MUS MUSCULUS (MOUSE), 703 aa (fragment).	2.4E-177	13
213	cg43933591	1167	ACATTTGGAATT TTAGCTTTTTTT IT[gap]GCCTCTC TACTGTGTCACT AAATAT	T gap	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q18476 C35A5.8 - CAENORHABDITIS ELEGANS, 1078 aa.	1.70E-176	8
214	cg43949875	2329	CTGAGTAGCTG GGATTACAGGC GTGTC/GCCAC CATGCCCAGCTA ATTTTTG	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34394 NUCLEAR PORE COMPLEX INTERACTING PROTEIN NP1P - HOMO SAPIENS (HUMAN), 350 aa.	6.60E-175	

215	cg43100840	1131	GGACAGGGGTG CAGCTGGCAGC CGA[G/A]AAAGG GGACCACCTCG GAGGGCTGG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P49752 HYPOTHETICAL PROTEIN ZAP113 - Homo sapiens (Human), 309 aa (fragment).	3.20E-168	
216	cg43922270	2077	TGTATATGTGTA CGTAGGTAGATG T[G/A]TGCAGCAT GCGGCAGGTTT GCCAGG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q14140 HYPOTHETICAL PROTEIN KIAA0127 - Homo sapiens (Human), 314 aa.	1.30E-162	2
217	cg43993462	1461	CAGAAATGAGCTG CAGAGGTTTCCT C[C/T]CTGCTTTA CAATCCCTTATT GAAGT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SP TREMBL- ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment).	5.10E-161	5
218	cg43993462	384	TAAACATCTACA GAGTTGAAACAT A[A/C]TCTGTCTAT ATTAAATATATTA TCTA	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SP TREMBL- ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment).	5.1E-161	5
219	cg43993462	624	TAGTCTCACTTC TTACCAAAAAA A[A/gap]CAATGA ACTGGATTTCAGC CCACTCA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SP TREMBL- ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment).	5.1E-161	5
220	cg43329741	996	GCAGTGCAGGA GATGACAGAGT GAG[G/A]AGGGC CCAGAGCAGAAT TCTGGCCC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD39906 FH1/FH2 DOMAIN- CONTAINING PROTEIN FHOS - HOMO SAPIENS (HUMAN), 1164 aa.	6.7E-159	
221	cg42910688	1687	AAACAATTTTGT TCAATGCCCACCC [G/A]AGACATATA GAATTGGGAAC GATA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P55040 GTP-BINDING PROTEIN GEM (GTP-BINDING MITOGEN-INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR) Homo sapiens (Human), 296 aa.	7.7E-158	8

222	cg43967474	969	TGCTGGGGACC ATGGATGGGA GGA[G/gap]GGG CACAGGGCCCA GTCAGATGAA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76848 KIAA1004 PROTEIN - HOMO SAPIENS (HUMAN), 496 aa (fragment).	1.70E-152	11
223	cg43964140	160	GCTGAGATCTTA GGTCAAAAAGCT AIC/TJAGAAAAGA AATCACTTTGAA AAACA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAC69899 SACM21 - MUS MUSCULUS (MOUSE), 721 aa.	1.10E-150	6
224	cg43990820	325	CCGGTTTAAAAG GAAAAGTAAAAA A[C/A]AATCCACA GTTGAGCAGTTG ATGTG	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q15024 MRNA (HA0800) FOR ORF - HOMO SAPIENS (HUMAN), 290 aa (fragment).	3.30E-150	3
225	cg43930377	682	TCACAGCTGGAT TGAAAGAGTATT T[G/A]GGAAATGT GGCAATGTTGTT TATAT	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43230 HYPOTHETICAL 33.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 290 aa (fragment).	7.80E-149	4
226	cg43969800	503	GCAAGACGTGT CAGGGGAACCA AGG[C/T]TCAGAT CATTCCCCCTTC ATCTACA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P25686 DNAJ PROTEIN HOMOLOG 1 (HSJ-1) - Homo sapiens (Human), 351 aa.	1.20E-145	2
227	cg43973724	2109	TATAAGTGTATG CAATAGAAATTT G[G/T]ATTTTGT ATAGAAAATTTA CCTTG	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75070 KIAA0483 PROTEIN - HOMO SAPIENS (HUMAN), 299 aa (fragment).	1.30E-141	1
228	cg43258867	112	GGCCCAAGTCCT GGGGCTCTGGG AGG[C/gap]TCAC GCTCCCTCCTCA GGCTGGGGA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99773 HYPOTHETICAL 30.9 KD PROTEIN - HOMO SAPIENS (HUMAN), 285 aa.	2.60E-141	

229	cg42907867	792	GACGATGTGGA CGCTGGGAGGG ATCT/gapJTGGC GTTGGTTTTCTG AAAGCCAGG	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99769 HYPOTHETICAL 26.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 255 aa.	1.10E-140	1
230	cg43920176	2819	AAAGCTGCTTTG TTAGGTTCCCTTA TIG/TTTTTATTAA CTGTCTTTTCTC AGTT	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD28325 LUMAN2 - HOMO SAPIENS (HUMAN), 272 aa.	1.40E-140	
231	cg43920176	2909	ATTTTGTCATTTT TTACATCAACTT[C/TATGGTCTTG TTTTTACATGGT AATT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD28325 LUMAN2 - HOMO SAPIENS (HUMAN), 272 aa.	1.40E-140	
232	cg43950100	856	CAAAATTAACAA ATTCACAAAATA C/A/GIACAGCTA GAATTACAAAAT CCATTC	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14681 PIG8 - HOMO SAPIENS (HUMAN), 318 aa.	1.70E-139	11
233	cg43950100	952	GGCACAGGGAG AAAAACAAAGTG TT[C/gap]CAATC AGTCCAGGCAC AGGGACTGG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14681 PIG8 - HOMO SAPIENS (HUMAN), 318 aa.	1.70E-139	11
234	cg43950100	391	ACATTGACCCCT TCAGTTCCTATA TIG/AICAGCACC CAATATTCTTT GAAATA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14681 PIG8 - HOMO SAPIENS (HUMAN), 318 aa.	1.70E-139	11
235	cg43950100	515	CAGGTTTAGTGT TGTTGTAGTGGC A/C/TJTTGTCCAG AATTGGTACCTC CCCAT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14681 PIG8 - HOMO SAPIENS (HUMAN), 318 aa.	1.70E-139	11

236	cg43132640	1317	CTCTATGAACTC TGTTTCTTTCTA [A/gap]TGAGATA TTAAACCATGTA AAGAAC	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P11226 MANNOSYL BINDING PROTEIN C PRECURSOR (MBP-C) (MBP1) (MANNAN-BINDING PROTEIN) (MANNOSYL-BINDING LECTIN) - Homo sapiens (Human), 248 aa.	4.20E-134	10 (10q11.2)
237	cg44938448	1310	TGAAAGTTAGAG AGCTGCAATCT CTT/gap]TAAGTAT CAATGTAAAGAA GCAGAT	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.80E-129	1
238	cg44938448	511	AATGCCACCTTC AGATGGAAGG AA[A/G]TGAGAT GGAAACAACAA AAAAGGA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.80E-129	1
239	cg43949897	923	AGCACTTTGGAG CTGGCCTCGCC CC[C/gap]TAGGA GGAGAGGGTCC CTCCTGGGT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60499 SYNTAXIN 10 - HOMO SAPIENS (HUMAN), 249 aa.	1.80E-126	19
240	cg42549778	1067	GGGGGTGCTCC TGGAAGCCCCA AGA[G/C]CATCC AGGATTGCCTCC CAGCTGCC	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD29690 PUTATIVE ZINC FINGER TRANSCRIPTION FACTOR OVO1 - MUS MUSCULUS (MOUSE), 267 aa.	3.70E-126	
241	cg44028574	990	CAGCTCCCAGCT ACCATGATGAGC C[C/gap]TGGCGG CTTGAGCACAGT GAGTGCT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD27724 CGI- 15 PROTEIN - HOMO SAPIENS (HUMAN), 329 aa.	4.00E-122	20

242	cg44035718	1088	TCTCATCTAGTG CTGAAGTCTGAG G[G/A]CTCTGCA GCATCAGACCCA CCTCTA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA83010 KIAA1058 PROTEIN - HOMO SAPIENS (HUMAN), 1534 aa (fragment).	2.20E-121	2
243	cg44035718	1172	GAAGAGAAAGAT AGGTTTAATTTAT T[T/C]TGAAGTTTT CATGGTGTTAAT ATTT	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA83010 KIAA1058 PROTEIN - HOMO SAPIENS (HUMAN), 1534 aa (fragment).	2.20E-121	2
244	cg43963595	1212	CCCCCGCAGAC AGAGGCCGGAG GCTT[G/T]CTGGT GCAGCGATGTTT AATGGCA	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75391 SPERM ACROSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 293 aa.	8.50E-120	17
245	cg43963595	1213	CCCCGCAGACA GAGGCCGGAGG CTT[T/G]CTGGTG CAGCGATGTTTA ATGGCAA	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75391 SPERM ACROSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 293 aa.	8.50E-120	17
246	cg43963595	1402	ATGTTACAGTAT GTACAAGACCCC T[C/gap]CCCTCG GGGACCGGGC GGACTCCG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75391 SPERM ACROSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 293 aa.	8.50E-120	17
247	cg43992566	492	AAATAGAGAATC CAGACCCCTCCC A[G/A]ATAATTTA AGAACTGAGTTT TCCTC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O14530 PROTEIN 1-4 - Homo sapiens (Human), 226 aa.	5.40E-118	
248	cg43992566	670	ATTAAATCTGA AGCAGAAAAAAA A[A/gap]GACAAT TTACAAAGAATT ATTGAGC	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O14530 PROTEIN 1-4 - Homo sapiens (Human), 226 aa.	5.40E-118	

249	cg43067745	907	TCCCTGCACGC CTTTACGTCAGA CTG/AJTCACCAC AAGAGCCTTGAG TGTCCA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.90E-118	
250	cg42697161	552	ACGTGGTGCTG GTAGTGTCTTGT TG/A/GJGTGTGA ATTCTCTCTCAT ACAAAAG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O15262 RING FINGER PROTEIN - HOMO SAPIENS (HUMAN), 247 aa.	1.00E-114	4
251	cg43957889	1466	GTGCAATGGCAT GATCTCGGCTCA C/C/TJGCAACCT CTGCCTCCCGG GTTCAAG	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00577 COSMID 6E5 CDK4, SAS AND KIAA0167 GENES, COMPLETE CDS, AND OS9 HOMO SAPIENS (HUMAN), 227 aa.	2.70E-111	12
252	cg42391024	404	AACTGCAGACAA ATTTCAAATTCA [C/AJTTCTTTACT TCTCCAAGATCT TCGA	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O43583 DRP1 PROTEIN (DRP) - Homo sapiens (Human), 243 aa.	4.30E-109	
253	cg43976566	711	CTTTAATGAAAC ACTTTGGATCGT C/A/GJGTGCTGA AGTGAAAGAAT GTGCTG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA74894 KIAA0871 PROTEIN - HOMO SAPIENS (HUMAN), 469 aa.	1.70E-107	4
254	cg44001900	936	GATGCTAAAAGC TTCTGCGAAATG T/G/AJTTACACGTT TAATGTTGGGAA ATCCC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA83057 KIAA1105 PROTEIN - HOMO SAPIENS (HUMAN), 730 aa (fragment).	1.20E-104	
255	cg43954569	471	TTCAGCCCCACAT GACTCAGGGAC AC[A/gap]CTCCC CAGCGGTTGCT GGAGGCACC	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P78560 DEATH DOMAIN CONTAINING PROTEIN CRADD (CASPASE AND RIP ADAPTATOR WITH DEATH DOMAIN) (RIP ASSOCIATED PROTEIN WITH A DEATH DOMAIN) - Homo sapiens (Human), 199 aa.	1.40E-101	12

256	cg43925519	791	AGTGCCCCCTTT CCCGCCCTGAA GAT/CJGTTTCAC ACGAAAAGGCC GTTTGTT	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P78317 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 190 aa.	4.40E-100	4
257	cg43145684	711	TGGCAAAACTGC CAGCAGCGGTT GC/C/TJGAAAT GCTGGGTTCGG TGCCTACT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA81666 DNA POLYMERASE ETA - HOMO SAPIENS (HUMAN), 713 aa.	2.90E-99	
258	cg43981803	626	ACCAGCTCGGA GAGGGCACTTG AGA/G/TJGGTCT ATGAACAAATCT GTCTAAAA	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16635 TFAZZIN - Homo sapiens (Human), 292 aa.	7.1E-97	X
259	cg44006111	1906	AGGCCTGATGC ACATGTGCACAG GT/A/GJCCTACAT GCTCTGTTCTTG TCAACA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:G1100182 T-CELL RECEPTOR BETA - HOMO SAPIENS (HUMAN), 311 aa.	3.8E-95	
260	cg44924968	1363	TGGCCAGGGAC CTGAGCCCCGAG ACA/C/TJCCCTG CATTGATCCAA CCAGGTCA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD43192 WUGSC:H_DJ0726N20.1 PROTEIN - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.8E-95	7
261	cg44924968	1364	GGCCAGGGACC TGAGCCCCGAGA CAC/C/TJCCCTGC ATTTGATCCAA CAGGTCAG	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD43192 WUGSC:H_DJ0726N20.1 PROTEIN - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.80E-95	7
262	cg43977021	1080	TTGCATCTAAAG TAATTCATTAAATG [T/A]ACAGGAGTA GATGAGGCCTG GCACA	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14206 ZAKI-4 MRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa.	9.20E-91	6

263	cg43977021	1087	TAAAGTAATTCA TTAATGTACAGG A[G/A]TAGATGA GGCCTGGCACA CATAGCA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14206 ZAK1-4 MRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa.	9.20E-91	6
264	cg43977021	1098	ATTAATGTACAG GAGTAGATGAG GC[C/T]TGGCAC ACATAGCAGAAG GTAATGG	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14206 ZAK1-4 MRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa.	9.20E-91	6
265	cg43977021	1107	CAGGAGTAGAT GAGGCCCTGGCA CAC[A/G]TAGCA GAAGGTAATGGT TCTATAGG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14206 ZAK1-4 MRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa.	9.20E-91	6
266	cg43977021	1116	ATGAGGCCCTGG CACACATAGCAG AA[G/A]GTAATG GTTCTATAGGTG TATCTTC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14206 ZAK1-4 MRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa.	9.20E-91	6
267	cg43977021	1169	TAATGCACCTTTG GGCTAGAGAAAT A[G/C]AAAAATCA CACGTAACAAAA ACAAA	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14206 ZAK1-4 MRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa.	9.20E-91	6
268	cg43999373	303	CACAGAAATTCAG AACTTTTTCACC C[G/C]GAACTGG AGAAGGAGCAC TCCGTCA	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88994 HYPOTHETICAL 38.2 KD PROTEIN - RATTUS NORVEGICUS (RAT), 338 aa.	1.50E-89	1
269	cg43980889	915	TTTGAGAGCTGC AGCAGAAAGCGG CT[G/T]TATCACA GACTGGATTAG TTATGA	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	4.5E-89	

270	cg43980889	936	GGCTGTATCACA GACTGGATTTAG T/T/GIATGATGAA AATACTGGACTG TATT	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	4.5E-89	
271	cg44030196	611	TAGATTGTTTCAG TACTCAGCTCAG C/A/gap]CCCAT AGACCATTTCTC CTCTGCG	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD40853 SIRTUIN TYPE 5 - HOMO SAPIENS (HUMAN), 310 aa.	7.4E-89	
272	cg40336929	317	GGCAACAAGTTA CAGCGGCGGGA GAT/A]GTTTCCT CTCTCACCTGCC GGGGG	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O73884 PUTATIVE PHOSPHATASE - GALLUS GALLUS (CHICKEN), 268 aa.	3.4E-84	
273	cg43920571	684	AGAAGACAGCG CGCAGAAATAGT GC[G/A]GAGAGA AATGACCAGTAG TATTAT	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P34624 HYPOTHETICAL 63.5 KD PROTEIN ZK353.1 IN CHROMOSOME III - Caenorhabditis elegans, 548 aa.	3.5E-82	10
274	cg43958980	537	TAAGATCCTCCA TCCCACCAAAAA T/A/G]ACCCACAA TGACTCCAAATC TTGTT	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43239 HYPOTHETICAL 41.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 383 aa (fragment).	4.50E-82	6
275	cg43320682	512	CATTGGCAACG GCTGCCCACTA GGG[G/gap]CACT GCCACTGCGCTG GCTCAAACT	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45773 HYPOTHETICAL 18.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 162 aa (fragment).	6.60E-81	
276	cg42708544	845	CCAGGCTTGCCTG CTAGATTGGCTG G[G/gap]CCAGAA TTTCTGGGGTCA GTCTGAA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14684 PIG12 - HOMO SAPIENS (HUMAN), 153 aa.	2.60E-79	

277	cg43949796	637	GGGAAGTAAAT C GAAGGAAGCAG AC/C/TTCCTTGCT CATCTTTCCAA TGAAAT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q94547 RGA AND ATU GENES, COMPLETE CDS - DROSOPHILA MELANOGASTER (FRUIT FLY), 579 aa.	1.20E-75	12
278	cg43298234	843	TAAGGCCAGAG A CTTGTGTGCTGG GC/A/gap/CAGAA ATCACCTGCTGC ATCCTGTG	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.30E-75	7
279	cg43926358	607	CAGTGATGTGCT A GGCCCTTTCAG GG/A/C/CACAGG CCCCTTCAGCTT CACCGGA	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75272 R33729_1, PARTIAL CDS - HOMO SAPIENS (HUMAN), 152 aa (fragment).	1.90E-74	19
280	cg35060315	1328	CCAAACTATCTC T ACCCACCCCTCC C/T/CJAGGATCC ACTTCCTTTGGAA TGACAA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P01225 FOLLITROPIN BETA CHAIN PRECURSOR (FOLLICLE- STIMULATING HORMONE) (FSH-B) - Homo sapiens (Human), 129 aa.	9.50E-73	11
281	cg35060315	1540	CTATTTTATCCAT A CCATGTTCTCCC [A/gap]AATCTGT GCTTCTTTTCAA CAGGTT	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P01225 FOLLITROPIN BETA CHAIN PRECURSOR (FOLLICLE- STIMULATING HORMONE) (FSH-B) - Homo sapiens (Human), 129 aa.	9.50E-73	11
282	cg35060315	1542	TTTTATCCATCC ATGTTCTCCCAA A/gap/AJTCTGTG CTTCTTTTCAAC AGGTTAT	gap	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P01225 FOLLITROPIN BETA CHAIN PRECURSOR (FOLLICLE- STIMULATING HORMONE) (FSH-B) - Homo sapiens (Human), 129 aa.	9.5E-73	11

283	cg35060315	1557	GTTCTCCCAAT CTGTGCTTTCTT TTC/TJACAGGTT ATATATTAAACT ATTT	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P01225 FOLLITROPIN BETA CHAIN PRECURSOR (FOLLICLE- STIMULATING HORMONE) (FSH-B) - Homo sapiens (Human), 129 aa.	9.5E-73	11
284	cg35060315	1562	CCCAAATCTGTG CTTCTTTCAAC AIG/CJGTATATA TTAAAACTATTTC ATGA	G	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P01225 FOLLITROPIN BETA CHAIN PRECURSOR (FOLLICLE- STIMULATING HORMONE) (FSH-B) - Homo sapiens (Human), 129 aa.	9.5E-73	11
285	cg44126579	18	TGTACAACTGAT TAGAGIAGapIGT TTTTTTTTCTT TTCCTTTTCAA	A	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P90839 F16A11.1 - CAENORHABDITIS ELEGANS, 673 aa.	1.1E-71	16
286	cg43951096	719	CCTCTCCTCCAA GAGTTGGTTCCG CIA/gapJAGAGGT GGAAAGAACTCT CAATAGT	A	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa.	2E-71	17
287	cg43951096	884	CACAGCCATAAT ATAGAGAACAGA GIC/gapJITCTCC ATGAACATCCAC CAGGCTG	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa.	2E-71	17
288	cg43960676	65	AGCAGCCAGCTT CATTGGCTGCAA AIC/TJGCCTCTCT CAGGTGAGTCAA AGGAG	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD43443 26S PROTEASOME SUBUNIT P40.5 - MUS MUSCULUS (MOUSE), 376 aa.	5.3E-69	

289	cg43323149	1101	TCACCTCAGATG AGTGTGGCTCC CC[C/G]CGCTCC CATACTGCAGCC TGCCCCCT	C	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1E-68	1
290	cg43969533	364	AAGGGAAGCCT ATCCTATTTTTT T[T/gap]TCCCTTG CGAAAACAGAAG CCAAGT	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD39844 HSPC028 - HOMO SAPIENS (HUMAN), 419 aa.	1.6E-67	7
291	cg43969533	365	AGGGAAGCCTAT CCTATTTTTTTTTT T/gap]CCTTTTGCG AAACACAGAAGCC AAGTT	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD39844 HSPC028 - HOMO SAPIENS (HUMAN), 419 aa.	1.6E-67	7
292	cg39376027	601	CCGGGGAGGTG GTTCTGGTAATC TG[G/T]GGGGGA GCCGGGACAGG CGCCCCGA	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD39515 HERMES - MUS MUSCULUS (MOUSE), 197 aa.	2.3E-66	
293	cg39376027	604	GGGAGGTGGTT CTGGTAATCTGG GG[G/T]GGAGCC GGGACAGGCGC CCCAGATT	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD39515 HERMES - MUS MUSCULUS (MOUSE), 197 aa.	2.3E-66	
294	cg43976681	210	CTCTCTCTTCGC CGCCGACGCAG AA[A/G]GGAGCT GGGAGGAAAA AGCTGCTG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD29427 MYOMEGALIN - RATTUS NORVEGICUS (RAT), 2324 aa.	4.3E-66	11
295	cg43085556	131	GTAAGGTAAAT GTGAATCAATAT G[T/C]TAGTTCTG GGCAATTATTCT GCAA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60223 SSX3 - HOMO SAPIENS (HUMAN), 188 aa.	8.8E-65	

296	cg43085556	149	CAATATGTTAGT TCTGGGCAATTA T/T/CJCTGCAAAT TCTGCCAGATAA TTAA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60223 SSX3 - HOMO SAPIENS (HUMAN), 188 aa.	8.8E-65	
297	cg43085556	150	AATATGTTAGTT CTGGGCAATTAT T/C/TJTGCAAAT CTGCCAGATAAT TAAAG	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60223 SSX3 - HOMO SAPIENS (HUMAN), 188 aa.	8.8E-65	
298	cg43085556	30	TGTTGTTCTCA AGCTTTTCGCCT A/C/TJATTTTGA CTAACCCCTGCTT ATTCC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60223 SSX3 - HOMO SAPIENS (HUMAN), 188 aa.	8.8E-65	
299	cg43085556	45	TTTTGCCTACA TTTTAGACTAAC C/C/TJTGCTTAT CCTGTGAATCAA GTGGT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60223 SSX3 - HOMO SAPIENS (HUMAN), 188 aa.	8.8E-65	
300	cg43085556	65	TAACCCCTGCTTA TTCCTGTGAATC A/A/CJGTGTGA TCTTCTGCAGCT TGGAA	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60223 SSX3 - HOMO SAPIENS (HUMAN), 188 aa.	8.8E-65	
301	cg43920089	437	GCATTGCTGCT TGTGCTTGATTT T/G/AJTTTGGCTC AATCCCTTCCTG GCAGC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14716 DNAJ PROTEIN - HOMO SAPIENS (HUMAN), 135 aa.	2E-63	
302	cg43950850	263	AAACATGTTCCA TCAAATTCAGAA A/C/gapJAGCAGG TATCAGTGAAC TGGAGCA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O95298 NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B) - Homo sapiens (Human), 119 aa.	7.8E-62	11

303	cg43950850	736	AGGAAACAC GACGACCACTAC CC[G/C]GGCCTA AGCGGTCAGCTT TCTCCTC	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O95298 NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B) - Homo sapiens (Human), 119 aa.	7.8E-62	11
304	cg44128084	1012	CATCCGCGCTG ACGGCAGTCAC CGG[T/C]GAGAC CGGCGCCGGA AGACCATGG	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa.	1.7E-59	
305	cg43976473	984	GACGCTCGCTG TCCCCGAGGGC CCG[gap/C]TGCG CCGCCCTGCTGG GTACGAATAC	gap	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O35946 HYPOTHETICAL 14.9 KD PROTEIN - RATTUS NORVEGICUS (RAT), 137 aa.	3.5E-59	11
306	cg44924858	546	GCTTCTGTCAGA CGTTACTTTTAC CIG/AJTGCCCTGC TGTTCCACAGG AAGAGT	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q12773 GUANINE NUCLEOTIDE REGULATORY PROTEIN - HOMO SAPIENS (HUMAN), 460 aa.	4.3E-59	
307	cg44924858	558	CGTTACTTTTAC CGTGCCCTGCTGT TTT/CJCCACAGG AAGAGTCTGTCT GTTCCA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q12773 GUANINE NUCLEOTIDE REGULATORY PROTEIN - HOMO SAPIENS (HUMAN), 460 aa.	4.3E-59	
308	cg44924858	755	ACCCAGCTTGCA CCGGCAGCAC CAI/A/GIACTGTT TCTTTGGCTTGA CGAATA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q12773 GUANINE NUCLEOTIDE REGULATORY PROTEIN - HOMO SAPIENS (HUMAN), 460 aa.	4.30E-59	
309	cg43961591	222	ACACCACTGGTA CTCACACCCCT CTT/CJGGCTGGG TTCTCTGGTGCG CCCTGC	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:O35414 STATHMIN-LIKE PROTEIN B3 (RB3) - Rattus norvegicus (Rat), 189 aa.	3.10E-58	

310	cg43924285	528	CTGCATATGTTT GCAGTTTTCCAT CIA/GIACITCTTC ATAAACAAACAA ACATT	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa.	4.20E-57	15
311	cg43924285	574	ACATTTTCTAGA AACCAAAATATG TIA/GITGGCCC AAAGGAGCTCTT AAGCAA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa.	4.20E-57	15
312	cg43958224	198	GTTTGATCCTCA GCCAGGACGCA CA[G/A]GCCCTA CAAGATCCCAGC CCTCCAA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43298 HYPOTHETICAL 13.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 118 aa (fragment).	2.30E-53	19
313	cg43971060	502	AACGGCTTTAAA CACAAAGCTCAG GG[G/gap]CTTGG GGTTATCCCGA GGGCACAG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P31639 SODIUM/GLUCOSE COTRANSPORTER 2 (NA(+)/GLUCOSE COTRANSPORTER 2) (LOW AFFINITY SODIUM-GLUCOSE COTRANSPORTER) - Homo sapiens (Human), 672 aa.	4.20E-53	
314	cg44927952	342	TATTTTCATTGT ACTTATTATTCAl T/C]TATACTTACT ATATATATTTAAA AC	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34077 CGI-82 PROTEIN - HOMO SAPIENS (HUMAN), 318 aa.	4.80E-52	
315	cg19885484	77	AAACAACAAAAT AACCAAAACATAA A/C]T]CAACTAAT GCTACACAGAAT GTGAT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15019 KIAA0301 - HOMO SAPIENS (HUMAN), 2047 aa (fragment).	1.90E-51	
316	cg42307356	11	CGGCCGCGGC[G/T]CGGAACGG CGCCTCCCGCC CCACCA	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15121 PUTATIVE FATTY ACID DESATURASE MLD - HOMO SAPIENS (HUMAN), 323 aa.	2.60E-51	

317	cg44005017	947	TGGGAGGCCTG GTTGCCCTCC GG[C/T]GTGCTG GGACACTCTGG GTTCTGTC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43363 HYPOTHETICAL 23.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 204 aa.	5.00E-51	
318	cg43329819	609	TTGAGCTCTCCT ACAAAGCTGGAG GC[A/C]AACAGT CAGTGAGAGCG GGGGGGCC	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92565 MYELOBLAST KIAA0277 - HOMO SAPIENS (HUMAN), 580 aa.	1.40E-50	
319	cg43329819	612	AGCTCTCCTACA AGCTGGAGGCA AA[C/T]AGTCAGT GAGAGCGGGG GGCCAGT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92565 MYELOBLAST KIAA0277 - HOMO SAPIENS (HUMAN), 580 aa.	1.40E-50	
320	cg43329819	625	GCTGGAGGCAA ACAGTCAGTGAG AG[C/T]GGGGG GCCAGTCAGAC CCGACCAA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92565 MYELOBLAST KIAA0277 - HOMO SAPIENS (HUMAN), 580 aa.	1.40E-50	
321	cg44015618	980	CAGCCTCATAGC CACACACACACA C[A/gap]CGTACC ACACACGCACAC ACACACA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75148 KIAA0658 PROTEIN - HOMO SAPIENS (HUMAN), 589 aa (fragment).	8.7e-312	11
322	cg44015618	1009	ACCACACACGCA CACACACACACA C[A/gap]CTTTGT GGCTCAAGTGC AGGCCACA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75148 KIAA0658 PROTEIN - HOMO SAPIENS (HUMAN), 589 aa (fragment).	8.7e-312	11
323	cg40361678	3074	CAACACTTTGGG AGGCCGAGGCA GG[T/C]GGATCA CCTGAGGTCAG GAGTTCTGA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:P14222 PERFORIN 1 PRECURSOR (P1) (LYMPHOCYTE PORE FORMING PROTEIN) (PFP) (CYTOLYSIN) - Homo sapiens (Human), 555 aa.	9.1e-313	

324	cg40361678	3144	GTGAACCCCGT CTCTACTAAAA TIA/TCAAAAATT AGCCGGGCATG GTGGCG	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:P14222 PERFORIN 1 PRECURSOR (P1) (LYMPHOCYTE PORE FORMING PROTEIN) (PFP) (CYTOLYSIN) - Homo sapiens (Human), 555 aa.	9.1e-313	
325	cg40361678	3161	CTAAAAATACAA AAATTAGCCGGG CIA/GITGGTGGC GGATGCCCTGTAA TCCCAG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:P14222 PERFORIN 1 PRECURSOR (P1) (LYMPHOCYTE PORE FORMING PROTEIN) (PFP) (CYTOLYSIN) - Homo sapiens (Human), 555 aa.	9.1e-313	
326	cg43930957	1287	AAATAAAACTC TTTTGAAAGTTG TIG/TGGTCAGC TGACCAGGTAGA GGATTC	G	T	Val	Val	Val	SILENT- CODING	apoptosi s	Human Gene Homologous to SPTREMBL-ID:Q62627 CLONE PAR- 4 INDUCED BY EFFECTORS OF APOPTOSIS - RATTUS NORVEGICUS (RAT), 332 aa.	1.6E-117	
327	cg43300636	413	CAAGGCGGCA AAGATGGGAC CAG/C/TJACCAC AGCGCCACGC CCACCTCCC	C	T	Val	Val	Val	SILENT- CODING	ATPase_ associated	Human Gene SPTREMBL-ID:Q29466 VACUOLAR H+-ATPASE SUBUNIT. (EC 3.6.1.34) H(+)-TRANSPORTING ATP SYNTHASE) H(+)- TRANSPORTING ATPASE) (MITOCHONDRIAL ATPASE) (CHLOROPLAST ATPASE) (COUPLING FACTORS (F(O), F(1) AND CF(1))) - BOS TAURUS (BOVINE), 838 aa.	1.7E-175	
328	cg43967912	749	CATTCTCTCTCC AAAAATTTCTCAG AT/CITTTGTGCAC AGGACTCCATT CAACC	T	C	Lys	Lys	Lys	SILENT- CODING	ATPase_ associated	Human Gene Homologous to SPTREMBL-ID:Q22494 SIMILAR TOS. CEREBISIAE VACUOLAR H(+)- ATPASE 54 KD SUBUNIT - CAENORHABDITIS ELEGANS, 470 aa.	5.6E-108	8
329	cg43967912	761	AAATTTCTCAG ATTTGTGCACAG G/A/G]CTCCATT CAACCTTCCAGA TTTAA	A	G	Ser	Ser	Ser	SILENT- CODING	ATPase_ associated	Human Gene Homologous to SPTREMBL-ID:Q22494 SIMILAR TOS. CEREBISIAE VACUOLAR H(+)- ATPASE 54 KD SUBUNIT - CAENORHABDITIS ELEGANS, 470 aa.	5.60E-108	8

330	cg43967912	773	ATTGTGCACAG GACTCCATTCCA A/C/TCTTCCAGA TTTAAAGTTCTGA ACTGT	C	T	Arg	Arg	SILENT- CODING	ATPase_ associate d	Human Gene Homologous to SPTREMBL-ID:Q22494 SIMILAR TOS. CEREBISIAE VACUOLAR H(+)- ATPASE 54 KD SUBUNIT - CAENORHABDITIS ELEGANS, 470 aa.	5.60E-108	8
331	cg43132502	371	AGTGGGTGGCA CCGCCGAGGCT GCTG/AJTTACG GCTCATCTTCAT TGATTTGC	G	A	Leu	Leu	SILENT- CODING	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa.	9.40E-58	11
332	cg44924856	352	ACACGCCCAGC AGCCGAATGATG TTT/GGGGTCCT TGAGCCTCGACA TGATCT	T	G	Pro	Pro	SILENT- CODING	cadherin	Human Gene Similar to SWISSPROT- ID:Q08345 EPITHELIAL DISCOIDIN DOMAIN RECEPTOR 1 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE CAK) (CELL ADHESION KINASE) (TYROSINE KINASE DDR) (DISCOIDIN RECEPTOR TYROSINE KINASE) (TRK E) (PROTEIN- TYROSINE KINASE RTK 6) - HOMO SAPIENS (HUMAN), 913 aa.	7.90E-77	6 (6q16)
333	cg43991318	2634	AGCACTCCCTGT GCTCACCCCTTCT C/T/CJCCCTCGTG GTCCCTTTTTCAC CTGGTG	T	C	Ser	Ser	SILENT- CODING	collagen	Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa.	1.30E-73	1 (1p34)
334	cg41553795	480	CTGTGCACGTG GTTGTCGCTGAG AC/C/TGACTACC AGAGTTTCGCTG TCCTGT	C	T	Thr	Thr	SILENT- CODING	complem ent	Human Gene Homologous to SWISSPROT-ID:P07360 COMPLEMENT C8 GAMMA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 202 aa.	1.40E-104	9 (9q34.3)
335	cg43973728	286	GCAAATTCAGAT GCAAAGCCGTG GC/C/TJAACGGG AAGGTTCTCCG AATGATC	C	T	Ala	Ala	SILENT- CODING	cyclin	Human Gene SWISSPROT- ID:P51946 CYCLIN H (MO15- ASSOCIATED PROTEIN) (P37) (P34) HOMO SAPIENS (HUMAN), 323 aa.	2.60E-172	5 (5q13.3)

336	cg43312829	1413	TCCAATCAAAGA CAACAGGACTCC AT/CIGTAACTGA ATATGAGGACAA TTTGA	T	C	His	His	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 617 aa.	0.00E+00	4
337	cg43312829	1422	AGACAAACAGGA CTCCATGTAAC GA/A/G]TATGAG GACAAATTTGAAG AAATCAT	A	G	Glu	Glu	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 617 aa.	0.00E+00	4
338	cg43312829	1452	AGGACAATTGGA AGAAATCATGGG TIA/GJTGGAAAG AGCTATATTCTG TTAGAA	A	G	Val	Val	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 617 aa.	0.00E+00	4

339	cg43312829	1473	GGGTATGGA GAGCTATATTCT GTT/CIAGAAATA TAAGGCCATCCT GCCACG	T	C	Val	Val	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 617 aa.	0.00E+00	4
340	cg43312829	1569	ACTGGATATTGA GAGGAATGGAG CC[G/A]TGGACT CTAAACATATAA GGCTCTG	G	A	Pro	Pro	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 617 aa.	0.00E+00	4
341	cg43312829	1623	TGAACGGCTCA AGCCAGCCCAAG GA/T/C]GTACAC CCATTGAGTATC CAAAAC	T	C	Asp	Asp	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 617 aa.	0.00E+00	4
342	cg43307992	652	TCGAGGGCCCC AACTTTGAGTTC TC/C/A]ACGGAG ACCCATGAGGA GCTGCTGT	C	A	Ser	Ser	SILENT- CODING	dehydrog enase	Human Gene Homologous to SPTREMBL-ID:O00217 MITOCHONDRIAL NADH DEHYDROGENASE-UBIQUINONE FE-S PROTEIN 8, 23 KDA SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 210 aa.	1.70E-113	11

343	cg43969759	965	TGGCTGTGGGC TTCACGAGCCTC AC/C/TJACCTCCT CCAGGGAGTTG ACTTCAG	C	T	Val	Val	SILENT- CODING	dehydrog enase	Human Gene Homologous to SPTREMBL-ID:Q16797 NADP- DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE) - HOMO SAPIENS (HUMAN), 572 aa.	1.80E-109	11
344	cg39523614	318	ATGCTGGATCAG ATCCAGCTGCAC T/A/TJAAGTGTG AGCCGACGAAG ATGGGG	A	T	Leu	Leu	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) - MYCOBACTERIUM LEPRAE, 389 aa.	2.10E-76	
345	cg39523614	360	AAGATGGGGAC AGTTTCGTCCTG AA/C/TJGGCGTC AAGGCTTGGGT CACGGAGG	C	T	Asn	Asn	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) - MYCOBACTERIUM LEPRAE, 389 aa.	2.10E-76	
346	cg39523614	366	GGGACAGTTTC GTCCTGAACGG CGT/C/TJAAGGC TTGGGTCACGG AGGCTGGCG	C	T	Val	Val	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) - MYCOBACTERIUM LEPRAE, 389 aa.	2.10E-76	
347	cg39523614	613	TCGAGGGCACG GTCTGAGTGTG CTT/TJTGCGTAC GCTTGACAACTC TCGTGT	T	C	Leu	Leu	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) - MYCOBACTERIUM LEPRAE, 389 aa.	2.10E-76	
348	cg39523614	660	GTGCTCGATTG CTGCTCAAGCAG T/G/AJGGAATTG CCCAGGGAGCT TTAGACA	G	A	Val	Val	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) - MYCOBACTERIUM LEPRAE, 389 aa.	2.10E-76	

349	cg42717491	207	AGGCTCACACTC ACTTCATGTTCT TTC/GIACAAAGTC CTCGCCTTTCTT GATGG	C	G	Val	Val	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P04636 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.1.1.37) - RATTUS NORVEGICUS (RAT), 338 aa.	2.40E-52	
350	cg42717491	252	TGATGGAGGCTT TCAGCTCAGGG ATG/AIGCCTCG GCAATCATTTTC TCCTCAA	G	A	Ala	Ala	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P04636 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.1.1.37) - RATTUS NORVEGICUS (RAT), 338 aa.	2.40E-52	
351	cg42717491	270	CAGGGATGGCC TCGGCAATCATT TTTC/TTCCTCAA AAGGAGTGATTT TGCCAA	C	T	Glu	Glu	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P04636 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.1.1.37) - RATTUS NORVEGICUS (RAT), 338 aa.	2.40E-52	
352	cg42717491	288	TCATTTTCTCCT CAAAAGGAGTGA TTTC/TTGCCAAT GCCTAGGTTCTT CTCCA	T	C	Lys	Lys	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P04636 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.1.1.37) - RATTUS NORVEGICUS (RAT), 338 aa.	2.40E-52	
353	cg42711596	1535	ATTAGTATGCT GTGAGCTGTCTT TTT/GJTTGAATC TGATTTAGTTTC AGTTC	T	G	Thr	Thr	SILENT- CODING	eph	Human Gene Homologous to SWISSPROT-ID:P48722 OSMOTIC STRESS PROTEIN 94 (HEAT SHOCK 70-RELATED PROTEIN APG-1) - MUS MUSCULUS (MOUSE), 838 aa.	2.10E-115	4

354	cg43319420	1557	AGAAGTCAGAAAG GCCTTCCTGTGG C/A/C/CCGTTTCAT GGACCGAGACA AAGTGA	A	C	Ala	Ala	SILENT- CODING	esterase	Human Gene Similar to SWISSNEW- ID:Q23917 3',5'-CYCLIC- NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa. pcls: SWISSPROT-ID:Q23917 3',5'- CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa.	3.30E-60	21
355	cg41029366	687	AGTGGGGATCA GTGTGCGATGA CACIT/CJTGGA CCTGGAGGACG CCCACGTGG	T	C	Thr	Thr	SILENT- CODING	glycoprot ein	Human Gene SPTREMBL-ID:Q61003 T CELL SURFACE GLYCOPROTEIN CD6 - MUS MUSCULUS (MOUSE), 665 aa.	1.00E-234	11
356	cg42876034	860	GCGCCCGCCGC GGCAGCGCCCC GAG/G/C/CCGGC TTCGGCCCCGCA GCCTGGACG	G	C	Gly	Gly	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q07066 22 KD PEROXISOMAL MEMBRANE PROTEIN - RATTUS NORVEGICUS (RAT), 193 aa.	2.60E-78	
357	cg43976227	258	CTGGTGTGATCT CTGTCTCTTTAT G[G/A]ACCACTA CTTTGGTCACTG ACATGT	G	A	Val	Val	SILENT- CODING	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	2.60E-60	18
358	cg43916642	816	GGCTGAAAAGC ATATCTATACATT C[G/A]GAGAAGT CGCAAATAGAAA GGAAAA	G	A	Ser	Ser	SILENT- CODING	helicase	Human Gene Similar to SWISSPROT- ID:P25888 PUTATIVE ATP- DEPENDENT RNA HELICASE RHLE - ESCHERICHIA COLI, 454 aa.	2.90E-54	1

359	cg43925670	2320	AACCAGCATCAC CTCGGAACCTTT C/T/C/TCCATCAA GTCAGCAATCTG AATTT	T	C	Glu	Glu	SILENT- CODING	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0.00E+00	1
360	cg43925670	2370	TTGTCATACTCT TCTCTCATTTT [A/G]ATTAAAGTTT TAAATCGTTGCT CAGT	A	G	Leu	Leu	SILENT- CODING	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0.00E+00	1
361	cg43925670	2389	TTTTAAATTAAG TTTTAAATCGTTI G/A/CTCAGTAAG GACTTAACCAT CTAA	G	A	Ser	Ser	SILENT- CODING	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0.00E+00	1

362	cg43925670	2446	AATCATTGATGA CCTCTAATCCTT TTT/CJAGTAGAAC AATGTTCTTGTA TTTTT	T	C	Leu	Leu	SILENT- CODING	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0.00E+00	1
363	cg44004587	1913	TTTTATTGTCATT TTCATCAATAAG[G/A]ATACACATC TCTGCCAGGAGT TGAA	G	A	Ile	Ile	SILENT- CODING	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3.00E-123	
364	cg43257400	2144	CATGTGTGGTAA CTCCTCAAGATG G[G/C]GAGACGT TAGCACAAATGA TAGAAG	G	C	Gly	Gly	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:Q60680 CONSERVED HELIX-LOOP-HELIX UBIQUITOUS KINASE - MUS MUSCULUS (MOUSE), 745 aa.	0.00E+00	10
365	cg43931272	2072	TTGGTGGTTCTT TCCCAACCACAA A[A/G]CACTCCG GTGGTAAATACC AATAAG	A	G	Cys	Cys	SILENT- CODING	kinase	Human Gene TREMBLNEW- ID:G2853031 TOUSLED-LIKE KINASE - MUS MUSCULUS (MOUSE), 717 aa.	0.00E+00	
366	cg42665067	748	GGGGCTTCTACA TATCCCCCGGAA G[C/T]ACCTTCAG CACTCTGCAGGA GCTGG	C	T	Ser	Ser	SILENT- CODING	kinase	Human Gene SWISSPROT- ID:P08631 TYROSINE-PROTEIN KINASE HCK (EC 2.7.1.112) (P59- HCK AND P60-HCK) (HEMOPOIETIC CELL KINASE) - HOMO SAPIENS (HUMAN), 526 aa.	9.20E-289	20 (20q11)

367	cg43982923	634	CGATGCAGAAAT ACGAGAAACTG GA/GAAGATT GGGGAAGGCAC CTACGGAA	A	G	Glu	Glu	SILENT- CODING	kinase	Human Gene SWISSPROT- ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.60E-159	19
368	cg43982923	655	TGGAAGAAGATTG GGGAAGGCACC TA/C/TJGGAACGTG TGTTCAAGGCCA AAAACC	C	T	Tyr	Tyr	SILENT- CODING	kinase	Human Gene SWISSPROT- ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.60E-159	19
369	cg43982923	697	CCAAAAACCGG GAGACTCATGAG AT/C/TJGTGGCTC TGAACCGGGTG AGGCTGG	C	T	Ile	Ile	SILENT- CODING	kinase	Human Gene SWISSPROT- ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.60E-159	19
370	cg43919086	576	CGCTCAGGAGG ATATAGGTGATG AC/A/GJCCGATG CTCCACATGTCC GCCTCCA	A	G	Gly	Gly	SILENT- CODING	kinase	Human Gene TREMBLNEW- ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa.	6.80E-158	19
371	cg25143358	407	GGCGGCTTCA AGTTTCGTGGTC AT/G/AJCCGCCG GTTCCCAACCCG GAACCCAG	G	A	Gly	Gly	SILENT- CODING	kinase	Human Gene Similar to SWISSPROT- ID:P46546 GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK) - CORYNEBACTERIUM GLUTAMICUM, 369 aa.	2.70E-51	

372	cg43105476	514	GGTCCGATGC CCCACATTGCTG GC/C/TGTGTGC TTCACCAGGAAC TCCACCA	C	T	Thr	Thr	SILENT- CODING	kinaseinh ibitor	Human Gene Similar to SWISSPROT- ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa.	7.80E-86	
373	cg43105476	541	TGTGCTTCACCA GGAACCTCCACCA C/C/AJCGGAGGT GGCCTTCTTTGG CAGCCA	C	A	Arg	Arg	SILENT- CODING	kinaseinh ibitor	Human Gene Similar to SWISSPROT- ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa.	7.80E-86	
374	cg43105476	595	GCAAGGGCAGG TTCCCTTCATTAT C/C/TJTCGATGT AACATCAGCTTG AAACT	C	T	Glu	Glu	SILENT- CODING	kinaseinh ibitor	Human Gene Similar to SWISSPROT- ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa.	7.80E-86	
375	cg43105476	616	TATCCTCGATGT TAACATCAGCTT G/A/GJAACCTCCA GCAAAGTCTGTA AAGTGT	A	G	Phe	Phe	SILENT- CODING	kinaseinh ibitor	Human Gene Similar to SWISSPROT- ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa.	7.80E-86	
376	cg43939695	410	CAGGGAACAGC AATGGGAACGC CAG/T/CJATCAAC ATCACGGACATC TCAAGGA	T	C	Ser	Ser	SILENT- CODING	kinasere ceptor	Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa.	0.00E+00	15 (15q25)
377	cg43939695	419	GCAATGGGAAC GCCAGTATCAAC AT/C/TJACGGACA TCTCAAGGAATA TCACTT	C	T	Ile	Ile	SILENT- CODING	kinasere ceptor	Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa.	0.00E+00	15 (15q25)

378	cg43939695	467	CTTCCATACACA TAGAGAACTGGC G/C/AJAGTCTTCA CACGCTCAACG CCGTGG	C	A	Arg	Arg	SILENT- CODING	kinasere ceptor	Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa.	0.00E+00	15 (15q25)
379	cg43939695	473	TACACATAGAGA ACTGGCGCAGT CTT/GJCACACG CTCAACGCCGT GGACATGG	T	G	Leu	Leu	SILENT- CODING	kinasere ceptor	Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa.	0.00E+00	15 (15q25)
380	cg43939695	479	TAGAGAACTGGC GCAGTCTTCACA C/G/AJCTCAACG CCGTGGACATG GAGCTCT	G	A	Thr	Thr	SILENT- CODING	kinasere ceptor	Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa.	0.00E+00	15 (15q25)
381	cg43939695	485	ACTGGCGCAGT CTTCACACGCTC AA/C/TGCCGTG GACATGGAGCT CTACACCG	C	T	Asn	Asn	SILENT- CODING	kinasere ceptor	Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa.	0.00E+00	15 (15q25)
382	cg43939695	509	ACGCCGTGGAC ATGGAGCTCTAG AC/C/GJGGACTT CAAAAGCTGACC ATCAAGA	C	G	Thr	Thr	SILENT- CODING	kinasere ceptor	Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa.	0.00E+00	15 (15q25)
383	cg43939695	518	ACATGGAGCTCT ACACCGGACTTC A/A/GJAAAGCTGA CCATCAAGAACT CAGGAC	A	G	Gln	Gln	SILENT- CODING	kinasere ceptor	Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa.	0.00E+00	15 (15q25)

384	cg29023997	183	TGGTTTCCATT TCAATCTGGATG G/G/A/TATGGAGC ACCATGTGCGCA CCTGCA	G	A	Gly	Gly	SILENT- CODING	kinasere ceptor	Human Gene SWISSPROT- ID:P36896 SERINE/THREONINE- PROTEIN KINASE RECEPTOR R2 PRECURSOR (EC 2.7.1.37) (SKR2) (ACTIVIN RECEPTOR-LIKE KINASE 4) (ALK-4) (ACTR-IB) - HOMO SAPIENS (HUMAN), 505 aa.	9.30E-280	12
385	cg43942537	2040	GTTCTTCTAGGG CCTGTAAACTT C/T/C/TTCACCTC TTCCTTAGAGGC ATCAT	T	C	Lys	Lys	SILENT- CODING	kinesin	Human Gene SWISSNEW-ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa.[pcls:SWISSPROT- ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00	10
386	cg43975720	2368	TCCGGAAGTGG AAGTGGTACCAG TTIC/TJACGTCTC TGCGGGACCTG CTGTGGG	C	T	Phe	Phe	SILENT- CODING	kinesin	Human Gene SWISSPROT- ID:Q12756 KINESIN-LIKE PROTEIN KIF1A (AXONAL TRANSPORTER OF SYNAPTIC VESICLES) - HOMO SAPIENS (HUMAN), 1690 aa.	0.00E+00	2
387	cg43975720	2398	CTCTGCGGGAC CTGCTGTGGG CAA/C/TJGCCATC TTCCTCAAGGAG GCCAATG	C	T	Asn	Asn	SILENT- CODING	kinesin	Human Gene SWISSPROT- ID:Q12756 KINESIN-LIKE PROTEIN KIF1A (AXONAL TRANSPORTER OF SYNAPTIC VESICLES) - HOMO SAPIENS (HUMAN), 1690 aa.	0.00E+00	2
388	cg43311943	44	TCGGGCCCGAT GACCCCAATGTG GC/G/CJAAAGACC AAGAACAACCTG GCTTCCT	G	C	Ala	Ala	SILENT- CODING	kinesin	Human Gene Similar to SWISSPROT- ID:Q05090 KINESIN LIGHT CHAIN (KLC) - STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN), 686 aa.	8.80E-51	
389	cg43311943	80	ACAACCTGGCTT CCTGCTACCTGA A/A/GJGAGGGCA AGTACCAGGATG CAGAGA	A	G	Lys	Lys	SILENT- CODING	kinesin	Human Gene Similar to SWISSPROT- ID:Q05090 KINESIN LIGHT CHAIN (KLC) - STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN), 686 aa.	8.80E-51	

390	cg43983535	4764	TCTCTGGGGCC CGCTGAGGTGA CAG[CT]AAGTG CTTTAGCTCCTG AGTCATAT	C	T	Leu	Leu	SILENT- CODING	laminin	Human Gene SWISSPROT- ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa.	0.00E+00	6 (6q22)
391	cg42488873	304	ATCCTTTGAAAA TCTCATATTGTTT [C/T]GAGTTTCA TTACTTCCATAC AAAG	C	T	Ser	Ser	SILENT- CODING	lipase	Human Gene SWISSPROT- ID:P54317 PANCREATIC LIPASE RELATED PROTEIN 2 PRECURSOR (EC 3.1.1.3) - HOMO SAPIENS (HUMAN), 469 aa.	9.80E-261	
392	cg43935885	3848	GGAAGCCCCAG CTGCAGGAGCT GCTTA/GJAAAGCT GCCCGCCTTCAT GCGGGTAA	A	G	Leu	Leu	SILENT- CODING	MHC	Human Gene SPTREMBL-ID:P79457 MALE-SPECIFIC HISTOCOMPATIBILITY ANTIGEN H- YDB - MUS MUSCULUS (MOUSE), 1186 aa.	7.20E-173	
393	cg44019843	955	ATGTGGAGTACA CCTTCACAGGGA TTC/TTACACCTT TGAGTCCCTCAT CAAGA	C	T	Ile	Ile	SILENT- CODING	misc_cha nnel	Human Gene SPTREMBL-ID:Q15478 SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 1836 aa.	0.00E+00	17 (17q23.1)
394	cg44929972	1266	ATGTCCTGAGG GCAGTGGAGGA ACG[G/A]GATTTT CCAACAGAAACC ATTAAAT	G	A	Arg	Arg	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.70E-214	7
395	cg44926604	1283	AGTCGATGTCCA GCTTGCGGGCC AC[G/A]CGGTGT AGATTGGGCAG GTTACAGCT	G	A	Arg	Arg	SILENT- CODING	nuclease	Human Gene SWISSPROT- ID:Q01831 DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XERODERMA PIGMENTOSUM GROUP C COMPLEMENTING PROTEIN) (P125) - HOMO SAPIENS (HUMAN), 939 aa.	0.00E+00	3

396	cg38642684	282	GCCAGTTAATAT TGCCTAGTAATT TTC/TGTGATAATC ATTTAAGGTATG TAAGT	C	T	Gln	Gln	SILENT- CODING	nuclease	Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcis:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	2.60E-50	
397	cg38642684	387	AAGGATACTTCC AAGGAGAGGAC ATT/CITGTACTT TTTCAGGTGCAA TGATTA	T	C	Gln	Gln	SILENT- CODING	nuclease	Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcis:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	2.60E-50	
398	cg38642684	405	AGGACATTGTGTA CTTTTCAGGTG CIA/TATGATTAA ACCACTTAACGT TGCAT	A	T	Ile	Ile	SILENT- CODING	nuclease	Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcis:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	2.60E-50	

399	cg38642684	456	TCCTTATGACAG AGGTATATAAAC TTT/CJAAAAGCAC TGGCTCCACTG GGGCTG	T	C	Leu	Leu	SILENT- CODING	nuclease	Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.jpcls:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	2.60E-50	
400	cg43919677	2577	TTGAAGTAGCTC CTGAAGCTTCTA CIG/ATCTAGTG CCAGCCAAAGTG ATTGCTC	G	A	Thr	Thr	SILENT- CODING	oncogene	Human Gene SWISSPROT- ID:Q00918 LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP- 1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT) - RATTUS NORVEGICUS (RAT), 1712 aa.	0.00E+00	2 (2p12)
401	cg44005163	1384	CCTGTGGGCTG ATTACATTAACT GAT/CJGCACAA AGATTATGTAAT GCTTTAT	T	C	Asp	Asp	SILENT- CODING	oncogene	Human Gene SWISSPROT- ID:P12756 SKI-RELATED ONCOGENE SNOA - HOMO SAPIENS (HUMAN), 415 aa.	5.30E-229	
402	cg44005163	1423	GTAATGCTTTAT TGCGGCCACGA ACIT/GJTTTCCTC AAAATGGTAGCG TACTTC	T	G	Thr	Thr	SILENT- CODING	oncogene	Human Gene SWISSPROT- ID:P12756 SKI-RELATED ONCOGENE SNOA - HOMO SAPIENS (HUMAN), 415 aa.	5.30E-229	
403	cg25334466	546	TCAAGGACCAGT TCACTACCCCTCC CIT/CJGAGGTGA AGGACTGATGCT TTGCCA	T	C	Pro	Pro	SILENT- CODING	oxidase	Human Gene Homologous to SWISSPROT-ID:P25689 URICASE (EC 1.7.3.3) (URATE OXIDASE) - PAPIO HAMADRYAS (HAMADRYAS BABOON), 303 aa.	1.30E-149	

404	cg42535091	750	AACTGAAATACG ACGTTGGTGGA GGIAGJGAACGG TTTGATTCTTTGA CAGATC	A	G	Gly	SILENT- CODING	phosphatase	Human Gene SWISSPROT-ID:Q06124 PROTEIN-TYROSINE PHOSPHATASE 2C (EC 3.1.3.48) (PTP-2C) (PTP-1D) (SH-PTP3) (SH-PTP2) - HOMO SAPIENS (HUMAN), 593 aa.	0.00E+00	12
405	cg43302847	1227	GGTGGTGGTGG CCATCCAGATCC TGIC/AJGGAAGA ACCCCAAAGGCT TCTTCTT	C	A	Arg	SILENT- CODING	phosphatase	Human Gene SWISSPROT-ID:P05186 ALKALINE PHOSPHATASE, TISSUE-NONSPECIFIC ISOZYME PRECURSOR (EC 3.1.3.1) (AP-TNAP) (LIVER/BONE/KIDNEY ISOZYME) (TNSALP) - HOMO SAPIENS (HUMAN), 524 aa.	3.20E-286	1 (1p36.1)
406	cg39728924	433	GGCAAAATGGTGT TGGAAAATAATT CIG/AJAAATGTTAT TGCCATGATAAC CAGAG	G	A	Ser	SILENT- CODING	phosphatase	Human Gene Similar to TREMBLNEW-ID:D1024666 PROTEIN-TYROSINE-PHOSPHATASE (EC 3.1.3.48) - MUS MUSCULUS (MOUSE), 426 aa.	1.20E-64	
407	cg42881873	1564	ACCTGAAAGCGAA GCGACTGGAAA GTIA/GJAACGGC GCGGGTCATAAA GTTAGCC	A	G	Val	SILENT- CODING	protease	Human Gene SWISSNEW-ID:P29122 SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-) - HOMO SAPIENS (HUMAN), 969 aa. ipclis:SWISSPROT-ID:P29122 SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-) - HOMO SAPIENS (HUMAN), 969 aa.	0.00E+00	15 (15q26)
408	cg42913398	589	CTGTTCCGTGGA TGAGAAAGATAGT CT/CJACATTTCT GAAATATTCTGC TCTTG	T	C	Val	SILENT- CODING	protease	Human Gene SPTREMBL-ID:O00199 INTEGRAL MEMBRANE SERINE PROTEASE SEPRASE - HOMO SAPIENS (HUMAN), 760 aa.	0.00E+00	2
409	cg44028327	793	TTCGAATTACCT ACTCAATTGTGC AIA/GIACGAATTG TTCCAAAGAGAA TTTTTC	A	G	Gln	SILENT- CODING	proteaseinhib	Human Gene SWISSPROT-ID:P01042 KININOGEN, HMW PRECURSOR (ALPHA-2-THIOL PROTEINASE INHIBITOR) (CONTAINS: BRADYKININ) - HOMO SAPIENS (HUMAN), 644 aa.	0.00E+00	3 (3q27)

410	cg43979831	899	CCTCAAGGACCA CTCCCAAAGACT TTC/TATGTTGA TGAGAACACAAC AGTCC	T	Phe	Phe	SILENT- CODING	protease inhib	Human Gene SWISSPROT- ID:P29622 KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4) - HOMO SAPIENS (HUMAN), 427 aa.	1.10E-228	14
411	cg43987538	905	ATCATCATAAGA GAAGAATCATTT TTT/AJCCAGTAGC CCCACCTACCATG AATGA	A	Gly	Gly	SILENT- CODING	reductase	Human Gene SWISSPROT- ID:Q08257 QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA- CRYSTALLIN) - HOMO SAPIENS (HUMAN), 329 aa.	1.10E-171	1 (1p31)
412	cg42717608	142	CCCACAAAGGTCT ATGTCCAGCACCC TTG/TCTGAAGA GAGACAAAGAAC ACCTGT	T	Leu	Leu	SILENT- CODING	reductase	Human Gene Similar to SWISSNEW- ID:P37040 NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR) - MUS MUSCULUS (MOUSE), 677 aa. pcis:SWISSPROT-ID:P37040 NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR) - MUS MUSCULUS (MOUSE), 677 aa.	1.80E-51	
413	cg43927378	4726	ATCTGATGGAGA ACTACCAGATCG TTT/CJGTCAGCAA CCTGGCCACTG AGCGTG	C	Val	Val	SILENT- CODING	struct	Human Gene SPTREMBL-ID:Q13459 MYOSIN-IXB - HOMO SAPIENS (HUMAN), 2022 aa.	0	2
414	cg43945592	1503	GGGCTCGGGCA GGGTACACAAAC TCTT/CJGTGGCT GCAAAATCCCCA GAGGAGC	C	Thr	Thr	SILENT- CODING	struct	Human Gene TREMBLNEW- ID:G2961252 SUPERVILLIN - HOMO SAPIENS (HUMAN), 1788 aa.	0	10
415	cg43957486	1475	CTGGGGCTCCC CGCTGCCAGTG CCC/A/GJGCCGG CGCCGCCCTGC AGGCAGACG	G	Pro	Pro	SILENT- CODING	struct	Human Gene SWISSPROT- ID:P07204 THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN) - HOMO SAPIENS (HUMAN), 575 aa.	0.00E+00	20 (20p11.2)

416	cg44932934	815	TGCTCGAGGAT GTCAACCGCATG TC[G/A]CCTGGG GCGCTGGCCAT TATCTTCG	G	A	Ser	Ser	SILENT- CODING	struct	Human Gene SPTREMBL-ID:Q63358 MYOSIN HEAVY CHAIN - RATTUS NORVEGICUS (RAT), 1980 aa.	2.10E-179	
417	cg43100187	320	AACGCCTAGAG GGGGAGCTGGT GGC[C/A]CATGA GCCTGCCATCCA GAATGTGC	C	A	Ala	Ala	SILENT- CODING	struct	Human Gene SWISSPROT- ID:P02549 SPECTRIN ALPHA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2418 aa.	1.80E-169	
418	cg42930605	333	GGTCCATGCACAG CCTTGCTCTCG AIG/AICCCAGCA GGCCCTTGAGC ATGGCAT	G	A	Gly	Gly	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)
419	cg42930605	411	GGGGCCGCTTG AACTGCCCCGC AG[A/G]TCAAATA GCTTCTGGTTCA TGTCCT	A	G	Asp	Asp	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)
420	cg42930605	435	GATCAAAATAGCT TCTGGTTTCATGT C[C/T]TCCAGCTC CTTGCTGGTCTT CTGCA	C	T	Glu	Glu	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)
421	cg42930605	477	TCTTCTGCACCC TCACCTCCCATGT C[G/A]TACTTCTC CTCTTCAGCCGC ATCGA	G	A	Tyr	Tyr	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)
422	cg42930605	507	TCTCCTCTTCAG CCGCATCGATCT T[G/C]GCGTGCA GCTGTTTGAGA GCTCCT	G	C	Ala	Ala	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)

423	cg42930605	516	CAGCCGCATCG ATCTTGGCGTGC AGC/TJTGTTGC AGAGCTCCTGCA CTTCAG	C	T	Gln	Gln	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)
424	cg42930605	528	TCTTGGCGTGCA GCTGTTTGCAGA G[C/T]TCCTGCA CTTCAGACATGG AGCCCG	C	T	Glu	Glu	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)
425	cg42930605	558	GCACTTCAGACA TGGAGCCCGGG ATTA/GJTGCAGC GGCGGGCAGTG CTCCGCCA	A	G	His	His	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)
426	cg42930605	564	CAGACATGGAG CCCGGGATATG CAG[C/A]GGCGG GCAGTGCTCCG CCAGGTAGT	C	A	Pro	Pro	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)
427	cg42930605	615	TCTGCTTCTCTG CCTCACGGCGG CT[C/T]TCCTCCT TCTCCAGCTCCG TGGCCG	C	T	Glu	Glu	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)
428	cg42930605	621	TCTCTGCCTCAC GGCGGCTCTCC TC[C/T]TCTCCA GCTCCGTGGCC GCTATCT	C	T	Lys	Lys	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)
429	cg42893961	51	AATGGCCAGCA GGAAGGCGGGG ACC[C/A]GGGGC AAGGTGGCAGC CACCAAGCA	C	A	Arg	Arg	SILENT- CODING	struct	Human Gene Similar to SPTREMBL- ID:Q01449 MYOSIN REGULATORY LIGHT CHAIN, CARDIAC MUSCLE ISOFORM - HOMO SAPIENS (HUMAN), 175 aa.	2.5E-89	

430	cg42475816	282	AATCAAGACAAA CCCGAATTGAAA A[G/A]AAGATTGA AGCCCACTTTGA TGCCA	G	A	Lys	Lys	SILENT- CODING	struct	Human Gene Similar to SPTREMBL- ID:Q10466 TITIN, HEART ISOFORM N2-B (EC 2.7.1.-) (CONNECTIN) - HOMO SAPIENS (HUMAN), 26926 aa.	7.3E-85	2 (2q24.3)
431	cg42522566	337	TGAAGAACGTAA AGGACCGGGAG GAT/CJGTGAAG AATGAGGTC AAC ATCATGA	T	C	Asp	Asp	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa.	6E-55	
432	cg43297806	953	GTAGATGGGTA GAATAGTAGCCA GG[G/A]ACAAGA CAGCGGTTCTG CAGGGAGC	G	A	Val	Val	SILENT- CODING	sulfotran sferase	Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa.	0.00E+00	10

433	cg43297806	962	TAGAATAGTAGC CAGGGACAAAG CA[G/A]CGGTTT TGCAGGGAGCG TAGTGCCA	G	A	Arg	Arg	SILENT- CODING	sulfotran sferase	Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa.	0.00E+00	10
434	cg43297806	973	CCAGGGACAAG ACAGCGGTTCTG CA[G/A]GGAGCG TAGTGCCAGAG GGGTCTGG	G	A	Leu	Leu	SILENT- CODING	sulfotran sferase	Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa.	0.00E+00	10

435	cg43297806	1004	GTAGTGCCAGA GGGGTCTGGGA GGA[G/A]GCTGA AATCACCTGATA GAAGGTAT	G	A	Ala	Ala	SILENT- CODING	sulfotran sferase	Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa.	0.00E+00	10
436	cg43297806	1016	GGGTCTGGGAG GAGGCTGAAATC AC[C/T]TGATAGA AGGTATAGTTCA GAGCAA	C	T	Gln	Gln	SILENT- CODING	sulfotran sferase	Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa.	0.00E+00	10

437	cg43297806	1019	TCTGGGAGGAG GCTGAAATCACC TGA/GJTAGAAG GTATAGTTCAGA GCAACTG	A	G	Tyr	Tyr	SILENT- CODING	sulfotran sferase	Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa.	0.00E+00	10
438	cg43297806	1028	AGGCTGAAATCA CCTGATAGAAGG T(A/G)TAGTTCAG AGCAACTGGGT CTCCAT	A	G	Tyr	Tyr	SILENT- CODING	sulfotran sferase	Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa.	0.00E+00	10

439	cg43297806	1043	GATAGAAGGTAT AGTTCAGAGCAA C/T/A/GGGTCTC CATGGGCTCGC TGATGCT	T	A	Pro	Pro	SILENT- CODING	sulfotran sferase	Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa.	0.00E+00	10
440	cg43297806	926	CAGAGGGGTAG TAAGTCAGCCAG CGT/CJTGTAGAT GGGTAGAATAGT AGCCAG	T	C	Gln	Gln	SILENT- CODING	sulfotran sferase	Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa.	0.00E+00	10
441	cg39515668	445	CAGCCACATTCC GGTAAGCCTCG CA/A/GIAGAGCC AGCTGGGCGCC AAGATACG	A	G	Leu	Leu	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCIN AMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa.	2.80E-72	

442	cg39515668	538	CGATGCCGAGG TTGTCGTCAATA CGIAGJATCATG CCGGCATCATTC GGCTGAG	A	G	Ile	Ile	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCIN AMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa.	2.80E-72	
443	cg39515668	580	TCGGCTGAGCG AGCACAGTATTG CCJAGJCGCACG AACCGGTCATAC TGGTCGG	A	G	Arg	Arg	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCIN AMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa.	2.80E-72	
444	cg39515668	655	GGGCGGAGCCA ACAAGGGGCCAG CAG[G/C]GCCCC AGCAAGACCCCTC ACCAGAGT	G	C	Ala	Ala	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCIN AMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa.	2.80E-72	
445	cg21428405	177	TGACCTCGCCAA TGACAGTGGCA GC[G/A]ACACCC CAATGGGCGCA GATCTCCA	G	A	Val	Val	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCIN AMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa.	2.20E-56	
446	cg21428405	273	CCTGGGACTCG CTCATGAGGATC TCIT/CITCAGGG GCGAGGTTCCG GTCGCGCA	T	C	Glu	Glu	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCIN AMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa.	2.20E-56	
447	cg21428405	327	GAACGCGGTCTG AGCTCGACGTG CAT[G/A]CCACC GTCGCCAGCAC TGGCCAGCT	G	A	Gly	Gly	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCIN AMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa.	2.20E-56	

448	cg38924050	301	TCTCGTTGATGA GGTCGTTACCCCT C/A/GICGGGTAC GTTACCCGACAC CGGCGA	A	G	Arg	Arg	SILENT- CODING	synthase	Human Gene Similar to SWISSPROT- ID:P50004 ATP SYNTHASE BETA CHAIN (EC 3.6.1.34) - STREPTOMYCES LIVIDANS, 477 aa.	2.60E-53	
449	cg38924050	310	TGAGGTCGTTAC CCTCACGGGTA CGT/CITCACCG ACACCGGCGAA AACCGAAG	T	C	Glu	Glu	SILENT- CODING	synthase	Human Gene Similar to SWISSPROT- ID:P50004 ATP SYNTHASE BETA CHAIN (EC 3.6.1.34) - STREPTOMYCES LIVIDANS, 477 aa.	2.60E-53	
450	cg38924050	352	AAACCGAAGTAC CGCCGAAAGTTGT G/G/CJCGGATAC GGTAAATCATCT CCTGAA	G	C	Ala	Ala	SILENT- CODING	synthase	Human Gene Similar to SWISSPROT- ID:P50004 ATP SYNTHASE BETA CHAIN (EC 3.6.1.34) - STREPTOMYCES LIVIDANS, 477 aa.	2.60E-53	
451	cg43925970	1703	GAGCACATAAG GTGAAGGTGGT GAC/T/AICCCAG AGAAGCGACCT CTATATAGG	T	A	Gly	Gly	SILENT- CODING	tm7	Human Gene SPTREMBL-ID:O00348 PUTATIVE ENDOTHELIN RECEPTOR TYPE B-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	9
452	cg41616031	1736	AAGGGATGTCC CCAAACTTCCAG TC/T/CJGAACGC CGCACATAGTAG TCCATCA	T	C	Ser	Ser	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P49019 PROBABLE G PROTEIN- COUPLED RECEPTOR HM74 - HOMO SAPIENS (HUMAN), 387 aa.	2.90E-214	12
453	cg41616031	1744	TCCCCAAACTTC CAGTCTGAACGC C/G/TJACATAGT AGTCCATCACGA ACGGC	G	T	Arg	Arg	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P49019 PROBABLE G PROTEIN- COUPLED RECEPTOR HM74 - HOMO SAPIENS (HUMAN), 387 aa.	2.90E-214	12
454	cg41616031	1796	GGCAGATGATCA GTAGAAAGTCAG CT/CJACTGCCA GGTTGAACAGG AAAATCC	T	C	Val	Val	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P49019 PROBABLE G PROTEIN- COUPLED RECEPTOR HM74 - HOMO SAPIENS (HUMAN), 387 aa.	2.90E-214	12

455	cg42489842	393	GGCTGGTCAAC ACAGGTCTTCTG AC[C/G]CTGCGC CAGATTGTTTTG AGCAAAG	C	G	Thr	Thr	SILENT- CODING	tm7	Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS SCROFA (PIG), 704 aa.	7.30E-106	
456	cg42489842	402	ACACAGGTCTTC TGACCCCTGCGC CA[G/A]ATTGTTT TGAGCAAAGTTG ATCAGT	G	A	Gln	Gln	SILENT- CODING	tm7	Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS SCROFA (PIG), 704 aa.	7.30E-106	
457	cg42489842	423	GCCAGATTGTTT TGAGCAAAGTTG A[T/C]CAGTCTCT TCATACCAACAC ATCGC	T	C	Asp	Asp	SILENT- CODING	tm7	Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS SCROFA (PIG), 704 aa.	7.30E-106	

458	cg42489842	432	TTTTGAGCAAAG TTGATCAGTCTC TTT/CJCATACCAA CACATCGCTGGA TGCTG	T	C	Leu	Leu	SILENT- CODING	tm7	Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS SCROFA (PIG), 704 aa.	7.30E-106	
459	cg42489842	456	TTCATACCAACA CATCGCTGGATG CTT/CJGCAAGTG AATATGCCAAAT ACTGCT	T	C	Ala	Ala	SILENT- CODING	tm7	Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS SCROFA (PIG), 704 aa.	7.30E-106	
460	cg42489842	471	CGCTGGATGCT GCAAGTGAATAT GC/C/TJAAATACT GCTCAGAAATAT TAGGAG	C	T	Ala	Ala	SILENT- CODING	tm7	Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS SCROFA (PIG), 704 aa.	7.30E-106	
461	cg42927358	947	TTTTGCTTTTG CAAACATCATCC T(G/A)ACAAATGG TCAGCCCAACAGA GGACA	G	A	Leu	Leu	SILENT- CODING	tm7	Human Gene Similar to SWISSPROT- ID:Q15391 PROBABLE G PROTEIN- COUPLED RECEPTOR KIAA0001 - HOMO SAPIENS (HUMAN), 338 aa.	1.40E-71	

462	cg42927358	544	ATGAATTTGACA CAATTGTCTTGC C[G/A]GTGCTTTA TCTCATTATATTT GTGG	G	A	Pro	Pro	SILENT- CODING	tm7	Human Gene Similar to SWISSPROT- ID:Q15391 PROBABLE G PROTEIN- COUPLED RECEPTOR KIAA0001 - HOMO SAPIENS (HUMAN), 338 aa.	1.40E-71	
463	cg32423505	1056	CCCTCCTCCTGG CTGAGAAAAAGT T[G/T]CCCTTGTG CAAAAACACTAG GTACC	G	T	Gly	Gly	SILENT- CODING	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	1.20E-55	3 (3q21)
464	cg43968711	2389	TATGATTGGATG TGGAAGAACTAT CIT/CJGTTGCAIT CACATTTAAACG ATTGG	T	C	Thr	Thr	SILENT- CODING	transcript factor	Human Gene SWISSPROT- ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
465	cg43297259	800	CTCCTGTGTGTG TCCTTAAGTGTG T[G/A]ATGAGGT GTGACTTCTGGC TAAAGC	G	A	Ile	Ile	SILENT- CODING	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. pcis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	7.80E-54	
466	cg20612302	301	TGGAGGCGGCC CACATGGCGGC CAC[C/G]GCCAT CCTCAACCTGTC CACGCGCT	C	G	Thr	Thr	SILENT- CODING	transcript factor	Human Gene Similar to SPTREMBL- ID:O08996 MYELIN TRANSCRIPTION FACTOR 1-LIKE - MUS MUSCULUS (MOUSE), 1182 aa.	1.70E-53	
467	cg43949162	856	GGGCCATGTTAA CCACTTCCTTTT G[C/T]TGATCATC TGGTTTTAAGAA AGGAT	C	T	Gln	Gln	SILENT- CODING	transferase	Human Gene Homologous to TREMBLNEW-ID:G2738933 GLUTATHIONE TRANSFERASE (EC 2.5.1.18) - HOMO SAPIENS (HUMAN), 222 aa.	1.30E-115	6

468	cg43928442	449	CATCCACATGGGC CCACGGTGATG GGC/AJAGCCCA AAGGCTCCGTAT CTGCAGG	A	Leu	SILENT- CODING	transferase	Human Gene Similar to SPTREMBL- ID:O09034 GLUTATHIONE S- TRANSFERASE SUBUNIT 13 - RATTUS NORVEGICUS (RAT), 226 aa.	2.60E-87	7
469	cg43976701	1859	GACAGCTCATTG GACTGTGTCAGA A/A/GJTTCGAGA ATATCATAAAGA TGACC	G	Lys	SILENT- CODING	transport	Human Gene SWISSPROT- ID:Q15436 PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM A - HOMO SAPIENS (HUMAN), 765 aa.	0.00E+00	
470	cg44005525	975	CTTGACTGTAA TATTACAATGAT A/G/AJATTCTTGT CCGAAATGTAAC CTTTG	A	Ile	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
471	cg44005525	1041	ATTCTGGTGTA AAGTGATATCGA G/A/GJAAGAATA CACCACCCTCAT ACACGG	G	Phe	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
472	cg44005525	1047	GTGTAAAAGTGA TATCGAGAAAGA A/T/GJACACCCAC CCTCATACACGG ATCCTG	G	Val	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	

473	cg44005525	1065	GAAAGAAATACAC CACCCCTCATACA CIG/AGATCCTG GAGGCCCTAGA ATGGTTG	G	A	Ser	Ser	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
474	cg44005525	1080	CCTCATACACGG ATCCTGGAGGC CC/T/CIAGAAATG GTTGATCTCCAT TCATAGA	T	C	Leu	Leu	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
475	cg44005525	1098	GAGGCCCTAGA ATGGTTGATCTC CA/T/CITCATAGA TGTATCGCCTT TGGGAC	T	C	Glu	Glu	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
476	cg44005525	1110	TGGTTGATCTCC ATTCATAGATGT TIA/GITCGCCTTT GGGACCAGCAC TGCAAT	A	G	Asp	Asp	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
477	cg44005525	1134	TATCGCCCTTGG GACCAGCACTG CAJA/GITTAGGT GGAGGGTCTAA AGTGATGT	A	G	Asn	Asn	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	

478	cg44005525	828	TGTTGGTCATAT ACTGAGTGGCAA TIA/GICTTCCAC CAAAGGGTCGG CAGGAT	A	G	Ser	Silent- Coding	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
479	cg17663981	225	CCGAGAAACCCG GGCACAGCGAG AGC/C/GJTG GTG CCAAGTGGCCC AAAAGTTCA	C	G	Ala	Silent- Coding	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.2 3)
480	cg17663981	234	CGGGCACAGCG AGAGCCTGGTG CCA/A/GJGTGGC CCAAAAGTTCAC GGCGGGCA	A	G	Gln	Silent- Coding	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.2 3)
481	cg42907760	1501	AACCTGAAGGC CAAAGTGTGAC TC/G/A/GACTCG GAGAGCACAGT CAGCCCCC	G	A	Ser	Silent- Coding	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0.00E+00	9 (9p12)
482	cg43301812	3795	CTCCATGGCTG GGATGCTCTGCT GC/G/A/JCTTGGT TTTGCCCCGAGTG GCAGCCT	G	A	Ser	Silent- Coding	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q93075 HYPOTHETICAL PROTEIN KIAA0218 - Homo sapiens (Human), 761 aa.	0.00E+00	3
483	cg43917756	1098	AGACACTGACCA CTGGGGGAGGT GC/A/GJGAGACT GTGCTGGATGTG GTGGAAA	A	G	Ser	Silent- Coding	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q14157 HYPOTHETICAL PROTEIN KIAA0144 - Homo sapiens (Human), 983 aa.	0.00E+00	1

484	cg43918356	2645	CATCTTCATCTA GAAACGCCCTCA CIG/TIGAAATGG AATTGCTGCCAG ACGTGG	G	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75176 KIAA0692 PROTEIN - HOMO SAPIENS (HUMAN), 783 aa (fragment).	0.00E+00	12
485	cg43924089	1031	CTGTGGTCCTCT CCACAGACAGG GT[C/T]CACATCA AACTGGGGGTG TCTCCAC	C	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA31589 KIAA0614 PROTEIN - HOMO SAPIENS (HUMAN), 1630 aa (fragment).	0.00E+00	12
486	cg43926428	2157	CAAACTTCATGA GATTGAAGATCT G[C/G]AGCTGCT GCTCCTTGAACA TGTCCTG	C	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:O14924 REGULATOR OF G- PROTEIN SIGNALING 12 (RGS12) - Homo sapiens (Human), 1447 aa.	0.00E+00	4
487	cg43950657	2478	CCTCTACCCATC GGTCAGTGTC CC[A/G]CCACCG GGGGGCTGCTG GGACTCTT	A	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q13009 T-LYMPHOMA INVASION AND METASTASIS INDUCING PROTEIN 1 (TIAM1 PROTEIN) - Homo sapiens (Human), 1591 aa.	0.00E+00 (21q22.1)	21
488	cg43955358	3560	CCCGACAATTGT ATCTGGCATAAA T[C/T]CCTTCACC CAGTAGATTAGG AATGA	C	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:P35573 GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA- GLUCANOTRANSFERASE (EC 2.4.1.25) (OLIGO-1,4-1,4- GLUCANTRANSFERASE) AMYLO- 1,6-GLUCOSIDASE (EC 3.2.1.33) (DEXTRIN 6-ALPHA-D- GLUCOSIDASE)] - Homo sapiens (Human), 1515 aa.	0.00E+00 1 (1p21)	
489	cg43970200	1374	CATTAGAGATCT GGGCTGCAAGG TC[C/T]CCTAACAT AATCAATAAACA GATTTT	C	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q92845 SMAP - HOMO SAPIENS (HUMAN), 792 aa.	0.00E+00	1

490	cg43970200	1629	TTAACTGTGGTA TACAGTCAGTGT AT/CIGCAAAACAT TGATTTAAAGCG GTCAT	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q92845 SMAP - HOMO SAPIENS (HUMAN), 792 aa.	0.00E+00	1
491	cg43999667	3688	GTACAGCCTGGT AATGGAGAAATCA A/A/GJTITTTGCTG TATCGTAAAGGC AGCAA	A	G	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O60281 KIAA0530 PROTEIN - HOMO SAPIENS (HUMAN), 1563 aa (fragment).	0.00E+00	6
492	cg44009187	6789	TCAACTTGCTCC AGTAGGCCGCC GGC/TJTCTGCA GGCAGCTCGGG CTGGAAGA	C	T	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P42858 HUNTINGTIN (HUNTINGTON'S DISEASE PROTEIN) (HD PROTEIN) - Homo sapiens (Human), 3144 aa.	0.00E+00	
493	cg44020180	3172	ATGGGTAGACTC GAGTTTGGTAAA T/G/AJTCCAAACC ATAGGCCACAAC CAAAC	G	A	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1
494	cg44020180	3177	TAGACTCGAGTT TGGTAAATGTCC A/A/GIACCATAG GCCACAACCAAA CAAGTG	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1
495	cg44020180	3199	CCAAACCATAGG A CCACAACCAAAAC A/A/TGTGGACTC CAGACCCGAGG GAGCTG	A	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1
496	cg44020180	3211	CCACAACCAAAAC A AAGTGGACTCCA G/A/GJCCCGAGG GAGCTGTGTAGA TACCTC	A	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1

497	cg44020180	3220	AACAAGTGGACT CCAGACCCGAG GGIACIGCTGTG TAGATACCTCGC ATTCGAG	A	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1
498	cg44020180	3226	TGGACTCCAGAC CCGAGGGAGCT GTG/AJTAGATAC CTCGCATTCGAG AAACTG	G	A	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1
499	cg44020180	3232	CCAGACCCGAG GGAGCTGTGTA GAT[A/G]CCTCG CATTCGAGAAAC TGCTCTGGT	A	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1
500	cg44020180	3247	CTGTGTAGATAC CTCGCATTCGAG A[A/G]ACTGTCTG GTTATAGTTGAT GAATC	A	G	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1
501	cg44020180	3289	TGATGAATCGCT CTGCGTGTATCT G[T/G]ACATCTG GAGAATACGGG ATTAAGT	T	G	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1
502	cg44020180	3298	GCTCTGCGTGTA TCTGTACATCTG G[A/G]GAATACG GGATTAAGTTCT CCTCTC	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1
503	cg44020180	3312	TGTACATCTGGA GAATACGGGATT A[A/G]GTTCTCCT CTCTGCTTTGTT CTGTT	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1

504	cg44020180	3319	CTGGAGAAATACG GGATTAAGTTCT C/C/TCTCTGCT TTGTTCTGTTGG GATCT	C	T	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1
505	cg44928323	2080	AGCAGGCAGAT AGAAAGTTCTGT CA/C/TCTCTCC TTTTTACGGGG TAGGAT	C	T	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:P97526 NEUROFIBROMIN - RATTUS NORVEGICUS (RAT), 2820 aa.	0.00E+00	17 (17q11.2)
506	cg44932392	1281	TGTCCTGGTTT TGATAAAATTGT T/G/A/AACTTATT GTTGAGATCAGC GCTGA	G	A	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD23581 CULLIN 2 - HOMO SAPIENS (HUMAN), 745 aa.	0.00E+00	
507	cg43991434	1266	TCTTGAGCAGAC CCATGTGCACGA G/G/C/JAGCCTGG TGAGGAAGGTG TTGGAGT	G	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:P46060 RAN-GTPASE ACTIVATING PROTEIN 1 - Homo sapiens (Human), 587 aa.	1.70E-304	22
508	cg43985955	1994	GCATGATAGGAT ATGGAATTCCTC C/A/T/JCAAATGG GAAGTGTTCCTG TAATGA	A	T	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	2.70E-299	
509	cg43985955	2009	GAATTCCTCCAC AAATGGGAAGTG T/T/A/JCCTGTAAT GACGCAACCAA CCTTAA	T	A	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	2.70E-299	
510	cg43985955	2021	AAATGGGAAGTG TTCCTGTAATGA C/G/A/JCAACCAA CCTTAATATACA GCCAGC	G	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	2.70E-299	

511	cg43985955	2060	TATACAGCCAGC CTGTCATGAGAC CT/GGCCAAACC CCTTTGGCCCTG TATCAG	T	G	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	2.70E-299	
512	cg44031765	2070	ACCTGCGCGTA GTAGATGTAGCG CA/G/AJCATGGA CTCGAAGGCCT GCCTGCTG	G	A	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14776 LZTR-1 - HOMO SAPIENS (HUMAN), 552 aa.	4.60E-279	22
513	cg43252100	466	TGCAGCCCGA GGTTCTTTTAC TC/C/AJATGGTAC CAAATGCAACTA TTCACC	C	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA83037 KIAA1085 PROTEIN - HOMO SAPIENS (HUMAN), 584 aa (fragment).	4.90E-278	
514	cg43934178	2445	CGATGCCATGCT TCTCCATGAGCG T/G/AJATGAGCTC GGCCTCCGTCA GGTAGT	G	A	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD29670 DNA TOPOISOMERASE III BETA - HOMO SAPIENS (HUMAN), 862 aa.	1.80E-274	
515	cg43031103	1696	ACATGGCCCTCC CCTTGGTTGAGG A/G/AJACAGCAG GGGCTGGTGTG AGGTGCA	G	A	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O60240 PERILIPIN - HOMO SAPIENS (HUMAN), 522 aa.	6.30E-266	
516	cg43258841	340	TAAATCTTGTGT GGCCATCATCCA G/T/GJGTGTGGA ACATTTCAACCGT CATCTT	T	G	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.70E-258	
517	cg43258841	358	CATCCAGTGTGT GGAACATTTTAC C/G/AJTCATCTTC TACTGGTATAAT TTGAA	G	A	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.70E-258	

518	cg43258841	370	GGAAACATTTAC CGTCATCTTCTA CT/GJGGTATAAT TTGAAAGTGCTT TATTT	T	G	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.70E-258	
519	cg43258841	388	CTTCTACTGGTA TAATTTGAAAGT GIC/TJTTTATTTT TGTCATGACTC ATTG	C	T	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.70E-258	
520	cg43258841	394	CTGGTATAATTT GAAAGTGCTTTA TT/CJTTTTGTCC ATGACTCATTGA CAGTA	T	C	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.70E-258	
521	cg43258841	403	TTTGAAAGTGCT TTATTTTGTGCC IAGITGACTCAT GACAGTACGAAA GTTT	A	G	His	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.70E-258	
522	cg43258841	421	TTTGTCCATGAC TCATTGACAGTA CIG/AJAAAGTTTT GGGGTTACTCTG ACTAT	G	A	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.70E-258	
523	cg43258841	484	AAACTCCATCCA CAAGTCCTTGCT G/A/GJATAATCAA TCGCTGAGCCTC ATCTC	A	G	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.70E-258	
524	cg43258841	493	CCACAAGTCCTT GCTGAATAATCA A/T/CJCGCTGAG CCTCATCTCTAG AAATTT	T	C	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.70E-258	
525	cg43971614	2529	TCACTTTCCTGT GGATTTCTTTCT G/T/CJCCGCTAGA CTGCATCTGCTG GCTTTC	T	C	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPPTREMBL- ACC:Q13283 GAP SH3 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 466 aa.	5.30E-253	5

526	cg43971614	2574	GCTTCCATTG AATCCAATCCCC C/A/GJTGACAT AAGAAGAGTTCT TTCCAT	A	G	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13283 GAP SH3 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 466 aa.	5.30E-253	5
527	cg43320405	916	TGTTCTTCAGGC CCTTCACCATGG A/A/GJGGCAGGA GGGCCCTTCACCT TGGCGG	A	G	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB46424 DKFZP434G153 PROTEIN - HOMO SAPIENS (HUMAN), 466 aa.	8.20E-245	
528	cg43922856	1667	TACTGGACCAT CTATACGAAAT G/T/CJTCTGAAGT TTCCACCCCTTT CCTTG	T	C	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa.	2.00E-237	12 (12q22)
529	cg43922856	1718	GAGTCTCTTG ACCTCTTGAG A/T/CJTCCCTAGT TAATGCCTGCAG AGGTC	T	C	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa.	2.00E-237	12 (12q22)
530	cg43991007	102	CAAGAGAACAG CAAGTGCACCAA AC/T/CJTAGCTGA AACAGAAAAAGA GACAGC	T	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75336 LIPRIN-BETA1 - HOMO SAPIENS (HUMAN), 1005 aa.	1.80E-236	
531	cg43940463	1709	GGCTCACCAGC TCCAGCTGCGT GTG/T/CJTCAATCC ACCACCAGCGT GTACTTGA	T	C	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q99771 JIP-1 - HOMO SAPIENS (HUMAN), 467 aa.	3.10E-232	
532	cg42676981	1712	GGAAGTAGAGG TCAGGTGGGGC TGT/G/AJGGGCT CTTCAGGTTCAA ACACCGGA	G	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P08910 PROTEIN PHPS1-2 - Homo sapiens (Human), 425 aa.	5.90E-231	15

533	cg43918561	843	GGAAGGAGGTC TACACCACGCTG AA[G/A]GGCCTC TACGCCACGCA CGCCTGCG	G	A	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P04177 TYROSINE 3- MONOOXYGENASE (EC 1.14.16.2) (TYROSINE 3-HYDROXYLASE) (TH) - Rattus norvegicus (Rat), 498 aa.	2.10E-224	11 (11p15.5)
534	cg43999712	566	ACGTACCAAAATG AAATGCTCTACG G[G/C]CGAATAG GCTACATCTATG CTCTGC	G	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O43813 SEVENTRANSMEMBRANE-DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.30E-221	2
535	cg43999712	569	TACCAAAATGAAA TGCTCTACGGG CG[A/C]ATAGGC TACATCTATGCT CTGCTTT	A	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O43813 SEVENTRANSMEMBRANE-DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.30E-221	2
536	cg43999712	659	GCCATATTCAGC AGATTTGTGAAA C[A/C]ATTTTAAAC CTCTGGAGAAAA CCTAT	A	C	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O43813 SEVENTRANSMEMBRANE-DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.30E-221	2
537	cg43922139	1860	ACTTGACTTTCC AGACACGGTGA GG[A/G]AGGAGG AGGCTGTCGGG ACCAAACG	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O88473 RJS - MUS MUSCULUS (MOUSE), 4836 aa.	2.80E-218	
538	cg43955639	512	CAGGCATGGTG ATGAGGGGTGC TGG[G/T]GCCAG GGAGGTGGCAG GAGCTGGCA	G	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O15417 CAGL79 - HOMO SAPIENS (HUMAN), 413 aa (fragment).	2.80E-215	
539	cg41022625	1066	GCCTGGCCATT GTCATCTTCTTC TC[T/C]GTGCTG GGCGTGGTCTTT GGCAAAAG	T	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34036 CGI-40 PROTEIN - HOMO SAPIENS (HUMAN), 845 aa.	2.00E-207	11

540	cg41022625	1102	TGGTCTTTGGCA AAGGGAACACG GC[G/C]TTCTGG ATCGTCTTCTCC ATCATTG	G	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34036 CGI-40 PROTEIN - HOMO SAPIENS (HUMAN), 845 aa.	2.00E-207	11
541	cg41022625	1111	GCAAAGGGAAC ACGGCGTTCTG GATC/TJGTCTTC TCCATCATTAC ATCATCG	C	T	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34036 CGI-40 PROTEIN - HOMO SAPIENS (HUMAN), 845 aa.	2.00E-207	11
542	cg44002669	1439	CCTTGGCGTTGC ACTCGCGGCAG CC[C/T]CTGTCCA GTTCCCTCCTTCT CCTTCT	C	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q16543 CDC37 HOMOLOG - HOMO SAPIENS (HUMAN), 378 aa.	8.80E-205	
543	cg43302693	702	GCCCCACCTGA GTGACAAATGATG TAT/TCTTGACCC CACCAGGGGTC GGCTCCA	T	C	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.70E-204	16
544	cg43921081	486	ACTTGGAAAGAA AGTATGCAGCG CTA/GJTACCAAG CCTCTCTTTGAC AAGAGAA	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q99733 NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 4 (NUCLEOSOME ASSEMBLY PROTEIN 2) (NAP2) - Homo sapiens (Human), 375 aa.	3.10E-202	11
545	cg42181143	1134	CACACCAGCGC TTCTGCCACTCC GAT/CJCCAAAG AAACTATGATCT TTGCTTT	T	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O15268 SKAP55 PROTEIN - HOMO SAPIENS (HUMAN), 359 aa.	2.80E-189	17
546	cg43918701	1667	TTTTCCAGATGC GACAGACATCAT TTT/CJGGGCATAT TCTAGAAACCAA GGGCA	T	C	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O60736 KE03 PROTEIN - HOMO SAPIENS (HUMAN), 367 aa (fragment).	1.10E-170	

547	cg43926685	815	AGAAATTCCTTAC TGGATCACCGCA A/C/T/AAGACCAT CCACAACGATTA CCGCA	C	T	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.50E-168	1 (1p36.33)
548	cg44927654	263	GTGCCAGCTTCT CCATGGTGCGCAT C/C/T/GTCAGGA TGCTGGGGTAG GGAGGTT	C	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74865 KIAA0842 PROTEIN - HOMO SAPIENS (HUMAN), 1020 aa (fragment).	7.3E-165	
549	cg43993462	2019	CCAACCTCATTGA CAGTGAGGGT GC/G/A/TCTCCA CTTCTGTTGGTG TAATTGA	G	A	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment).	5.1E-161	5
550	cg44010310	1180	CTATATTCCTG ATTGTGCAAGT A/C/T/AAGACATT ATATTCGACATC TTTGG	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA32101 BCAP - HOMO SAPIENS (HUMAN), 331 aa.	1.3E-155	13
551	cg43950590	1319	GGTGACCATGT ACAGCTGCCCAA T/C/T/TGAGAGAA GAATCCTCCGAC GGCTT	C	T	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa.	1.9E-154	7
552	cg43950590	1334	GCTGCCCAATCT GAGAGAAAGAATC C/T/C/CCGACGG CTTCGTTACCAT CCTGTC	T	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa.	1.90E-154	7
553	cg43950590	1361	CGACGGCTTCG TTACCATCCTGT CT/G/A/AAGCGG ATTGCACGAGCC CAGTAAT	G	A	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa.	1.90E-154	7

554	cg43950590	1370	CGTTACCATCCT GTCTGAAGCGG ATT/GIGCACGA GCCCAGTAATTG CCCCATT	T	G	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa.	1.90E-154	7
555	cg43950590	1376	CATCCTGTCTGA AGCGGATTGCA CGIA/GJGCCAG TAATTGCCCCAT TCAATCA	A	G	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa.	1.90E-154	7
556	cg43950590	1397	CACGAGCCCG TAATTGCCCCAT TCIA/GJATCATGG TTCCTGGTCGGA GTTGGT	A	G	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa.	1.90E-154	7
557	cg43950590	1436	GTCGGAGTTGGTA AAGACCTGAGTT CIA/GJTATATATT AGGTCGGGATCT TGGCA	A	G	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa.	1.90E-154	7
558	cg43950590	1445	GGTAAGACCTGA GTTCATATATATT IA/GIGGTCCGGA TCTTGGCACAGG CTCAT	A	G	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa.	1.90E-154	7
559	cg43951092	1484	GAGTAGAATTCA AGAAGAGTTCAA TIA/GJTATCGATG TTGCATGTTATTT TTAT	A	G	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa.	4.50E-152	14
560	cg43951092	1526	TATTTTATCTTT AGACATGGCAG CIT/CJACTGCATC TTCATGTGTGCAC AAACT	T	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa.	4.50E-152	14

561	cg43951092	1583	CTGCTTCTCTCTG TGGCTCTGCCAT C/A/GGCTCCAA TATCAATATGAA CTCGTA	A	G	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa.	4.50E-152	14
562	cg43951092	1604	CATCAGCTCCAA TATCAATATGAA C/T/GJCGTATTG GATTTAGTGGTG AGAAGA	T	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa.	4.50E-152	14
563	cg43951092	1616	TATCAATATGAA CTCGTATTGGAT T/T/GJAGTGGTG AGAAGAAATTAG CAATGT	T	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa.	4.50E-152	14
564	cg43951092	1640	TTAGTGGTGAGA AGAAATTAGCAA T/G/AJTCATTTTC AGTTGCACGAAA AGGCA	G	A	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa.	4.50E-152	14
565	cg43990820	1135	CATCAGTTTCCA CTTCGACACATC G/G/AJTAGTCCT CACAGCCACGG CCATCCA	G	A	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q15024 MRNA (HA0800) FOR ORF - HOMO SAPIENS (HUMAN), 290 aa (fragment).	3.30E-150	3
566	cg43990820	724	TCGACCCCTCTT CATCCTCCAAAA C/T/CJCGAACCC TTGGTATCCTTG TATTGA	T	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q15024 MRNA (HA0800) FOR ORF - HOMO SAPIENS (HUMAN), 290 aa (fragment).	3.30E-150	3
567	cg43986914	319	TCAGGAAAAGGA AGCATGACAAAT T/C/TJCCACATAA CCAAAGAAGAGA AGGGA	C	T	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q99598 TRANSLIN- ASSOCIATED PROTEIN X (TRANSLIN-ASSOCIATED FACTOR X) - Homo sapiens (Human), 290 aa.	2.10E-148	

568	cg43119818	1245	AAGAAATTATCA ATGTGGGGCATT C/T/CJTTCATGT AAATTTTGAGGA CAACG	T	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P00915 CARBONIC ANHYDRASE I (EC 4.2.1.1) (CARBONATE DEHYDRATASE I) - Homo sapiens (Human), 260 aa.	6.90E-141	8 (8q22)
569	cg44027444	681	CAGTGCCAGAG TCCAGGAACTGA ACI/A/GITCAAGA GCCCGGCTGCT GTGAACAT	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA76379 TUDOR REPEAT ASSOCIATOR WITH PCTAIRE 2 - HOMO SAPIENS (HUMAN), 468 aa (fragment).	2.50E-129	9
570	cg29351416	429	CCACACAGGAC ACTGTGGTGGC CCTT/CJGATGCT CTGTCCAAATAC GGAGCAG	T	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa.	3.20E-127	
571	cg29351416	435	AGGACACTGTG GTGGCCCTTGAT GC/T/CJCTGTCC AAATACGGAGCA GCTACTT	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa.	3.20E-127	
572	cg29351416	546	AGTCCAAGTAG ACAACAGTAATC G/C/TJCTGTACT GCAGCAGGTCT CATTAC	C	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa.	3.20E-127	

573	cg29351416	645	TGTATGCTCAGAC CCACGCTGAGAT A/C/TJACATGCC CTTGAGAAAGCA GCAGC	T	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa.	3.20E-127	
574	cg29351416	648	ATGCTCAGACCA CGCTGAGATACA A/C/TJATGCCCTT GGAGAAGCAGC AGCCTG	T	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa.	3.20E-127	
575	cg43950273	530	GGTCTTCAATAA AGTAGTTATGGC A/C/AJGTCCTGAT CCACATAGATAG CTGAA	A	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB45700 HYPOTHETICAL 32.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 287 aa (fragment).	2.40E-123	
576	cg44930828	555	TCAACACAAGGC AGCCACAGGCC AA[A/G]ATCATTG TATTGGGTTTGT TACCTC	G	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa.	3.10E-122	

577	cg44930828	564	GGCAGCCACAG GCCAAATCATT GT[A/G]TTGGGTT TGTTACCTCGAG GTGAGA	A	G	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa.	3.10E-122	
578	cg44930828	591	TGGGTTTGTAC CTCGAGGTGAG AA[A/G]CCCAATC CTTTGAGGCAAA AGAACG	A	G	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa.	3.10E-122	
579	cg44930828	597	TGTTACCTCGAG GTGAGAAACCCA ATT/CJCCCTTTGAG GCAAAAGAACG CCAAGG	T	C	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa.	3.10E-122	

580	cg44930828	603	CTCGAGGTGAG AAACCCAATCCT TTTG/AIAGGCAAA AGAACGCCAAG GTGAACC	G	A	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa.	3.10E-122	
581	cg44930828	615	AACCCAATCCTT TGAGGCCAAAAGA AIC/TIGCCAAAG TGAACCAACTCC TCAAGG	C	T	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa.	3.10E-122	
582	cg44930828	630	GGCAAAAGAAC GCCAAGGTGAA CCA/A/GJCTCCT CAAGGTTTCGCT GCCGAAGC	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa.	3.10E-122	

583	cg44930828	645	AGGTGAACCAAC G TCCTCAAGGTTT C[G/C]CTGCCGA AGCTTGCCAACG TGCAGC	C	Ser	Silent- Coding	UNCLASSIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa.	3.10E-122	
584	cg44930828	663	AGGTTTCGCTGC C CGAAGCTTGCCA A[C/T]GTGCAGC TCCTGGATACCG ACGGGG	T	Asn	Silent- Coding	UNCLASSIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa.	3.10E-122	
585	cg44930828	690	TGCAGCTCCTG T GATACCGACGG GGG[T/C]TTGTG CACTCGGACGG TGCCATCT	C	Gly	Silent- Coding	UNCLASSIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa.	3.10E-122	

586	cg44930828	693	AGCTCCTGGATA CCGACGGGGT TTT/CJGTGCACT CGGACGGTGCC ATCTCCT	T	C	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa.	3.10E-122	
587	cg43975478	691	AAAACCCCTGAGA AAAGATACAATG TTC/TJCTGGGAG CTGAGACTGTGC TCAATC	C	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q63555 SP120 - RATTUS NORVEGICUS (RAT), 798 aa.	4.10E-119	
588	cg42530218	601	GCATGCCCAGTA ATAAAGATGAAG A/T/CJGGGCTAG TGGTTTTAGTTTT CAACA	T	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P70582 NUCLEOPORIN P54 - RATTUS NORVEGICUS (RAT), 510 aa.	2.00E-118	
589	cg43122111	248	AGTGGTGGATC CCCAGGAGGAG GAG[C/A]GAAGG CGGGCAGGTGG CGGGGCAGA	C	A	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O43770 BCL7C PROTEIN - HOMO SAPIENS (HUMAN), 217 aa.	5.00E-115	
590	cg43986282	656	CTTTTGGCCCAT ACTTCITTCGGT AIG/AICAGGATTT GCAGTAGATCTC TTCAT	G	A	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12
591	cg43986282	683	AGGATTTGCAGT AGATCTCTTCAT CIG/AJTGAAATTGC CACTGTTGTGCT ATCTA	G	A	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12

592	cg43986282	704	CATCGTGAATTG CACTGTTGTGC TIA/GITCTAAAT TTTCCTGCAAC CATGC	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12
593	cg43986282	731	CTAAATTTTCTC GCAAACCATGCA IG/CIAGAAAGCA GCAGGGTGGA AGCTCC	G	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12
594	cg43986282	757	AGAAAGCAGCA GCGGTGGAAGC TCCIT/GJGCCAT CACACTGCACCT CTTCTGCG	T	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12
595	cg43986282	779	TCCTGCCATCAC ACTGCACCTCTT CIT/AJGCGTGT ACACGGTCCTCC CACAGG	T	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12
596	cg43986282	794	GCACCTCTCTGT CGTGGTACACG GTIC/TJCTCCAC AGCCCCACAC TTGTTTC	C	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12
597	cg43986282	800	CTTCTGCGTGGT ACACGGTCCTCC CIA/GJCAGGCCC CACACTGTTTC CACCTC	A	G	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12
598	cg43986282	809	GGTACACGGTC CTCCACACAGC CCC/A/GJCACTT GTTCCACCTCC CCAGACAG	A	G	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12

599	cg43986282	815	CGGTCTCTCCCA CAGGCCCCACA CTT[G/A]TTTCCA CCTCCCAGACA GGCATTG	G	A	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12
600	cg42723058	651	GTCCTTACCACT CACCGGTCACA GAT[C/G]TGAGC CTTGAGTTGCAG CAGCTGC	T	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA82158 HCR PROTEIN - HOMO SAPIENS (HUMAN), 756 aa.	1.70E-107	
601	cg42723058	673	AGATGTGAGCCT TGAGTTGCAGCA GIC/TJTGCGGA AGAACGGAACC GCCTGGA	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA82158 HCR PROTEIN - HOMO SAPIENS (HUMAN), 756 aa.	1.70E-107	
602	cg43981269	727	AGATGGCTGGC CAGATGGGCAT GTT[C/T]AACCCG ATGCCATCCCT TTCGGGG	C	T	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q91579 RIBONUCLEOPROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 462 aa.	4.50E-105	
603	cg43972159	1381	TAGGTTCTCGGG CTGCTGAACGTG T[C/A]GATTTTGA CTTTCTTTCTCC TTGC	C	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa.	2.60E-102 (12q24.1)	7
604	cg43972159	1390	GGGCTGCTGAA CTGTCGATTTT GA[C/T]TTTCTT TCTCCTTGCTGT CTGTCA	C	T	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa.	2.60E-102 (12q24.1)	7
605	cg43972159	1420	CTTCTCCTTGC TGTCTGTACAG G[A/C]ACCCACCT AAATATCCTCAG GGACG	A	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa.	2.60E-102 (12q24.1)	7

606	cg43972159	1426	CCTTGCTGTCTG TCACAGGAACCC A/C/TJTAAATAT CCTCAGGGACG TGTCAC	C	T	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa.	2.60E-102	7 (12q24.1)
607	cg43972159	1465	GGGACGTGTCA CCCACAGTCAC CA/C/TJTCTTCT CCCATTTCCGCA CTTTCT	C	T	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa.	2.60E-102	7 (12q24.1)
608	cg43972159	1522	CGCCCATCACCT TCCTGATGTCAT C/C/TJTTGGCC GGCTACGGGTC TCGGCCC	C	T	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa.	2.60E-102	7 (12q24.1)
609	cg44911139	722	GCAAGGTTCCG GATGACGTATC AT/C/TJTCAGATC GGAACCTCACGTC GTTCTA	C	T	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14499 SPLICING FACTOR - HOMO SAPIENS (HUMAN), 530 aa.	7.90E-101	14
610	cg42539705	165	AAACGGAACAT TTCCAGATGAGG C/G/AJGGGTGTC TGGGAGGGGCT GTGGGTG	G	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75229 R31449.3 - HOMO SAPIENS (HUMAN), 813 aa (fragment).	1.20E-100	
611	cg42028329	115	CCAAGGAGAAC CCGTGCAGAAAA TT/C/TJCAGGCCA ACATCTTCAACA AGAGCA	C	T	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
612	cg42028329	277	ACTTTGACAACC CAGTACACCGGT C/T/AJCGGAAAT GGCAGCGACGG TTCCTCA	T	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	

613	cg42028329	295	ACGGGTCTCGG AAATGGCAGCG ACG[G/A]TCTTC ATCCTTTACGAG CACGGCC	G	A	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
614	cg42028329	310	GGCAGCGACGG TCTTCATCCTTT AIC/TGAGACG GCCTCTTGGCT ACGCCC	C	T	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
615	cg42028329	316	GACGGTCTTCA TCCTTTACGAGC AIC/TGGCCTCTT GCGCTACGCC TGGATG	C	T	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
616	cg42028329	328	TCCTTTACGAGC ACGGCCTCTTGC GIC/AITACGCC TGGATGAGATGC CCACGA	C	A	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
617	cg42028329	352	GCTACGCCCTG GATGAGATGCC CAC[G/C]ACCCT TCCTCAGGGCA CCATCAACA	G	C	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
618	cg42392719	540	TCGCGAGAACG GCCTCAGTGCC AAG[G/T]CCCTTA CCCCTGCAGCT GGGCTCTG	G	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43370 HYPOTHETICAL 23.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 206 aa.	6.40E-99	
619	cg42392719	606	TCTCCCCAAGG TGGGGTCTTCTA GIA/GTCTGTGA GGAAGAGGTTT ACATCTC	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43370 HYPOTHETICAL 23.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 206 aa.	6.40E-99	

620	cg42392719	627	CTAGATCTGTGA GGAAGAGGTTT AC/A/GTCTCCCA CCATGCAGCTCT CTTCAG	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43370 HYPOTHETICAL 23.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 206 aa.	6.40E-99	
621	cg39512856	597	ACGCGTCGCCG GAAGCCACGTC ATA/G/AJACGGTT TTACCCCGATGG TCTTCAA	G	A	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	
622	cg39512856	615	CGTCATAGACG GTTTTACCCCGA TG/G/AJTCTTCAA CGAGATGCCAC GATGCCT	G	A	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	
623	cg39512856	663	CCTCATCACTGT TGAAAACAGCCA C/A/GJAAAGCCAG CCGGAATATCTG GCGGTG	A	G	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	
624	cg39512856	690	AGCCAGCCGGA ATATCTGGCGGT GC/A/GJATATCG GTA CTGTTTGCA GGCAGAC	A	G	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	
625	cg39512856	708	GCGGTGCAATAT CGGTACTGTTTG C/A/TJGGCAGAC CGGTATGAGGC GGAATAT	A	T	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	
626	cg39512856	717	TATCGGTACTGT TTGCAGGCAG CC/G/TJGTATGA GGCGGAATATAT GCGTCAC	G	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	

627	cg37445474	599	CCCTGCAAGCTC TGTATGGAACGA TTC/TCCCCAGAT CTTTGGGAAAGG AGAAT	C	T	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q63615 VACUOLAR PROTEIN SORTING HOMOLOG R-VPS33A - RATTUS NORVEGICUS (RAT), 597 aa.	2.80E-96	
628	cg30791729	294	CAGATCCAGTG GCCTTCCCCCA GCT/G/TGTCAA CTGTGTCCAGG CTGTGGCT	G	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P12346 SEROTRANSFERRIN PRECURSOR (SIDEROPHILIN) (BETA-1-METAL BINDING GLOBULIN) - Rattus norvegicus (Rat), 698 aa.	3.20E-95	
629	cg42522690	454	GTGAACAGTGTA AATCAGTTTTTC AT/CITGGGACAT GAAATCCAAGGA TAAGG	T	C	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O35884 NEBULIN-RELATED ANCHORING PROTEIN (N-RAP) - MUS MUSCULUS (MOUSE), 1175 aa.	3.30E-94	10
630	cg42522690	625	CTCGAAAGTCTC TTGGTGAGGAAT AT/CJACAGAAAG CTATGAGCAACC CAGGG	T	C	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O35884 NEBULIN-RELATED ANCHORING PROTEIN (N-RAP) - MUS MUSCULUS (MOUSE), 1175 aa.	3.30E-94	10
631	cg43982164	561	AGGTCTACGTGT TGAAGCGTCCTC AT/CJGTGGATG AGTTCCTGCAGC GAATGG	T	C	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15194 HYA22 - HOMO SAPIENS (HUMAN), 340 aa.	1.00E-90	
632	cg43980889	755	AAGACCAATTAC AAGTAGAAAATG AT/CJGCTTACCC TGGTACCGATAG AACAG	T	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	4.50E-89	
633	cg43980889	770	TAGAAAATGATG CTTACCCTGGTA C/C/TGATAGAAC AGAAAATGTTAA ATATA	C	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	4.50E-89	

634	cg43980889	776	ATGATGCTTACC CTGTACCGATA G/A/GIACAGAAA ATGTTAAATATA GACAAAG	A	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	4.50E-89	
635	cg43980889	791	GTACCGATAGAA CAGAAAATGTTA A/A/GJTATAGACA AGTGGACCATTT TGCCT	A	G	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	4.50E-89	
636	cg43955651	449	CTTCCACCACGC CTGTGTTCTGGG C/G/AJCTGACAA AGGCCACCTTGT TGGTGT	G	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27745 CGI-36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa.	1.10E-87	2
637	cg43955651	476	TGACAAAGGCCA CCTGTTGGTGT C/G/AJGGCTTGA GGCGAATGAAG CCACACT	G	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27745 CGI-36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa.	1.10E-87	2
638	cg42353267	1516	GGCCTTCGATCC AGTCCATGAGCA A/T/CJGCCATATA GCGCGGCGCAG AGAGCT	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75249 R26660_1, PARTIAL CDS - HOMO SAPIENS (HUMAN), 291 aa (fragment).	2.60E-86	
639	cg37027086	258	GGGTTCTTCAAC TGGGACAGGAG GC/T/CJCTACCC ACCAGGCCCAA AACGAGG	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA78824 KIAA0980 PROTEIN - HOMO SAPIENS (HUMAN), 1406 aa (fragment).	1.20E-83	
640	cg42688841	449	TCAACATAAGGT AGAAATTTCAATTA A/C/TJCTCAAGAA GCGAGCGTCAT AGTATA	C	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGDH SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (Cl- SGDH) - Bos taurus (Bovine), 189 aa.	1.90E-83	

641	cg42688841	454	ATAAGGTAGAAT TTCATTAAACCTC A/A/GIGAAGCGA GCGTCATAGTAT AAAGAA	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGDH SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (Cl- SGDH) - Bos taurus (Bovine), 189 aa.	1.90E-83	
642	cg42688841	461	AGAAATTCATTA ACCTCAAGAAGC G/A/GJGCGTCAT AGTATAAAGAAG GCTTGA	A	G	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGDH SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (Cl- SGDH) - Bos taurus (Bovine), 189 aa.	1.90E-83	
643	cg42688841	476	TCAAGAAGCGA GCGTCATAGTAT A/A/GIGAAGGC TTGACGACAAAC AGTCTCT	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGDH SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (Cl- SGDH) - Bos taurus (Bovine), 189 aa.	1.90E-83	
644	cg43982291	1590	CACTGTGACCAT TTTGTACAGCAA G/A/CJAGCAGCG GTATATTCCCAT CCAAAT	A	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q28282 C3VS PROTEIN - CANIS FAMILIARIS (DOG), 659 aa.	3.20E-79	
645	cg43982291	1716	GTAAGCTGTTT TCCCAGAGCTGT C/G/AJACACTTTC GGCTGGGCATTT AGACT	G	A	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q28282 C3VS PROTEIN - CANIS FAMILIARIS (DOG), 659 aa.	3.20E-79	
646	cg44003673	320	CATGCTGGTGCA CTGGTGCCAGG TG/A/GJGTGATG ACGACCTCCAC GGCCTGCA	A	G	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD25021 CALCIUM- REGULATED HEAT STABLE PROTEIN CRHSP-24 - HOMO SAPIENS (HUMAN), 147 aa.	1.60E-77	

647	cg44003673	449	CATCAGAGATGT GCAGGAAGATG TC[G/A]GGCCG CCATCAGCTGG GGTAATGA	G	A	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD25021 CALCIUM- REGULATED HEAT STABLE PROTEIN CRHSP-24 - HOMO SAPIENS (HUMAN), 147 aa.	1.60E-77	
648	cg44003673	470	TGTCGGGGCCG CCATCAGCTGG GGT[A/G]ATGAA GCCATGGCCCTT GGACCCGC	A	G	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD25021 CALCIUM- REGULATED HEAT STABLE PROTEIN CRHSP-24 - HOMO SAPIENS (HUMAN), 147 aa.	1.60E-77	
649	cg44936941	1207	CGCGCACCTCG TCGCCGATCTGC TG[T/C]CCGGTC TCCTTGCCGAG GAAGTCGT	T	C	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62630 SM-20 - RATTUS NORVEGICUS (RAT), 355 aa.	7.00E-77	1
650	cg39523553	704	GGTGTGCCCCG TCCGGGATGGC TGC[C/A]GGTGG GTGATCGACGG TAGGCCGGA	C	A	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.20E-75	
651	cg39523553	721	ATGGCTGCCGG TGGGTGATCGA CGG[T/C]AGGCC GGACAATGCC CGGCCCGTC	T	C	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.2E-75	
652	cg39523553	772	GAGGACAGCCA TGGAAGGGCAC GGA[T/C]CGCCA GTGCCGGGGCG TGATTATGG	T	C	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.2E-75	
653	cg39523553	823	ACGTGGTGCGC AACAGCCCTCAC GG[A/G]GTGAAG GTCCAGATGGCT CTTCCG	A	G	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.2E-75	

654	cg39523553	874	CCTGGCCCGAG CTCGATCAGGCA TCIA/GIAGGTGC CTGGAATCCTTA CTCGATG	A	G	Ser	Silent- Coding	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.2E-75	
655	cg39523553	886	TCGATCAGGCAT CAAGGTGCCTG GAIA/GITCCTTAC TCGATGACGGTT TAGTGC	A	G	Glu	Silent- Coding	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.2E-75	
656	cg36728314	399	GCTGCTGCTTCT TCCTTGTGGCAA CIG/AIATCTTCTG GGCAACGTCCT GGAAGA	G	A	Ile	Silent- Coding	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83051 KIAA1099 PROTEIN - HOMO SAPIENS (HUMAN), 804 aa.	1.3E-73	
657	cg41677120	375	TTCAGTGCACAA ATGAGATGAATG TIG/TJACATCCC ACAGTTGGCAGA CAGTT	G	T	Val	Silent- Coding	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	1.10E-71	11
658	cg44126579	655	AGGAGTATTTCAT CATCCCCAATGC CIG/AITAGCCTTC ATGATTGAGGAA TTTGC	G	A	Tyr	Silent- Coding	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P90839 F16A11.1 - CAENORHABDITIS ELEGANS, 673 aa.	1.10E-71	16
659	cg44126579	712	GAGTGGCCCGAG CCAATCTGCATG ACIG/AJCCAGAA GTGACCACTGTT ACTTCAT	G	A	Gly	Silent- Coding	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P90839 F16A11.1 - CAENORHABDITIS ELEGANS, 673 aa.	1.10E-71	16
660	cg38925480	73	AGAACTCACCA GCCTTGTGGTGC TIG/AICATTTGCA TAACAACCGCAT CCAGC	G	A	Leu	Silent- Coding	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75473 ORPHAN G PROTEIN- COUPLED RECEPTOR HG38 - HOMO SAPIENS (HUMAN), 907 aa.	4.90E-69	

661	cg43323149	544	GCACCAGCGGA AGCCCTACAGAC GGIAGJCTCAGC GTCATGCAAGG GCCCTACA	A	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
662	cg43323149	559	CTACAGACGGA CTCAGCGTCATG CAIAGJGGCCCC TACAGCGAAACA GCCAGCT	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
663	cg43323149	664	GAAAATACAGCC GGTTAGAAATTC AIAJGJGCCGATG TCCAAAAGGAAA TTTTCC	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
664	cg34243633	263	CCACCACAGAG ATAATGCAGGCC AGIGCJGAGGAG ATTGCACTGGAT GTCACCA	G	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa.	1.3E-68	
665	cg34243633	431	CAACTGCTGTCA CAATGCTGGCAC CIGAIACATAAGA ACTTGTTTTCCA GCTGG	G	A	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa.	1.3E-68	
666	cg34243633	482	GGAGCAGCATG GCAACCCAGTGT GCCIC/TJAAAAG CCCCAGAAGGC CTAGGATGT	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa.	1.3E-68	
667	cg43942922	231	AGCCACATCTC AGGCCACTAGG GGIC/AJAGAACA AATAGGTCCTCT GTCAAGA	C	A	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.3E-68	

668	cg43942922	291	CAGTTGTCCCCA CAGCCCCCTGAG CTC/TTCAGCCTT CCACCTCCACAG ACCAGC	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.3E-68	
669	cg43942922	396	CTGTCAAGACCC CTGAACAGTTG TIG/CJCCACAG CCCCTGAGCTC CAGCCTT	G	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.3E-68	
670	cg43955219	1090	CCTGGCCAACAT GGCAAAACCCC GTTC/TTCTACTA AAATACAAAA GCCGGG	C	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	6.4E-68	
671	cg29142822	401	CACTCACAAAA GGGCAAGAAGC GC/A/GJAGGAGG GATAATGTCTTG GAAGCCA	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q07320 ZEIN-ALPHA PRECURSOR (ZSF4C4) - ZEA MAYS (MAIZE), 266 aa.	2.5E-65	
672	cg43988710	397	TGGTGAAGAG GTTGTACAGCAC TC/G/TJTAGTGTA GACTTCAGGTCA CAGTTG	G	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34051 CGI-56 PROTEIN - HOMO SAPIENS (HUMAN), 317 aa.	1.4E-62	
673	cg43988710	404	AGAGGTTGTACA GCACTCGTAGTG T/A/GIGACTTCAG GTCACAGTTGAC AATGT	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34051 CGI-56 PROTEIN - HOMO SAPIENS (HUMAN), 317 aa.	1.4E-62	
674	cg39516123	1049	GCTTGGACCGG CATGTGGCCTAT GGT/CJGGCTAT TCTACCCCGGA GGATCGGA	T	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa.	5.1E-62	

675	cg39516123	452	CAGGCAGCCTG GGACAGCCAG CCC[G/A]TCTGC CCAGAGAAACTA CCAGAGCT	G	A	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa.	5.1E-62	
676	cg39516123	563	TCAGTCTCTCTC CGGAAAGCCAG GC[C/T]CGAGCT CAGTTCAGTGTG GCTGGCG	C	T	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa.	5.1E-62	
677	cg39516123	620	CGGTGCCTGGG AGCCCTCAGGC GCG[C/T]CACAG AACAGTGGGCA CCAACACTC	C	T	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa.	5.1E-62	
678	cg42731307	435	GGAATGAGCC AAAGTTCGCATG AA[T/C]CCACGG AAGTTTACCTGG TCCTCTC	T	C	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa.	2.6E-61	
679	cg44128084	440	CCGGACAACAC CGTTGGAGTTCT TT[T/C]GCCGTCA ACGAGTTGTCTC TGGAAA	T	C	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa.	1.70E-59	
680	cg44128084	665	TGAGCGCTCAC GCTCTCTTTGCT CGIAGJCCGCTG GTCATGAGCCCA GCTGCTC	A	G	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa.	1.70E-59	
681	cg44128084	680	TCTTGCTCGAC CGCTGGTCATGA G[C/T]CCAGCTG CTCGAGTGGAC CTTGACA	C	T	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa.	1.70E-59	

682	cg44128084	695	TGGTCATGAGCCG CAGCTGCTCGA GT[G/A]GACCTT GACATCCAGCCA GACGGTT	G	A	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa.	1.70E-59	
683	cg44128084	728	ACATCCAGCCAG ACGGTTCAGAA C[A/G]GCGGTTT TGTGGTGGGAC GGGCGCC	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa.	1.70E-59	
684	cg30455661	289	CCACATACACAA CAGCATATACCT T[C/T]CCTGGGAT TCTCAAAGTGGT TGAAG	C	T	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14185 DOCK180 PROTEIN - HOMO SAPIENS (HUMAN), 1865 aa.	5.20E-58	
685	cg30455661	347	GATTCAACAGA AGAAATCAGCCC T[C/T]TGGAGAT GCCATAGAAACC ATGGA	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14185 DOCK180 PROTEIN - HOMO SAPIENS (HUMAN), 1865 aa.	5.20E-58	
686	cg30455661	382	CCATAGAAACCA TGGAGCTGACC AA[C/T]GAGAGG ATCAGCAACTGT GTTGAGC	C	T	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14185 DOCK180 PROTEIN - HOMO SAPIENS (HUMAN), 1865 aa.	5.20E-58	
687	cg43302460	827	AGCTCGGAGT ACAGGTGAAACT TC[T/G]CGAATTG CCTGTTCTTCT TTCTGA	T	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43289 HYPOTHETICAL 12.7 KD PROTEIN - HOMO SAPIENS (HUMAN), 116 aa (fragment).	1.70E-57	2
688	cg43153425	101	AAGGCCGACTTT CTGTAGGAAAGTA A[C/T]TCGTGACC GAGAGATCAGC ATGCTCTG	C	T	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment).	2.40E-57	

689	cg43153425	107	GACTTCTGTAG GAAGTAACCGTG A/C/TTCGAGAGA TCAGCATGTCTG TCGGTC	C	T	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment).	2.40E-57	
690	cg43153425	128	GTGACCGAGAG ATCAGCATGTCT GTIC/TJGGTCTG GGAAGGTCACA GTTAGACT	C	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment).	2.40E-57	
691	cg43153425	140	TCAGCATGTCTG TCGGTCTGGGA AG[G/A]TCACAG TTAGACTCCAAA GGAGGAG	G	A	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment).	2.40E-57	
692	cg43153425	146	TGCTGTCTGGTC TGGGAAGGTCA CA[G/A]TTAGACT CCAAAGGAGGA GTAGTTG	G	A	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment).	2.40E-57	
693	cg43153425	152	TCGGTCTGGGA AGGTCACAGTTA GA[C/T]TCCAAAG GAGGAGTAGTT GGTGGGA	C	T	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment).	2.40E-57	
694	cg43153425	155	GTCTGGGAAGG TCACAGTTAGAC TC[C/T]AAAGGA GGAGTAGTTGGT GGGACCA	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment).	2.40E-57	
695	cg43153425	251	CAAAATCAGCAAC CAAACCAACAAA TAT/CAAAATTAC TATGGGTTCTAC TGAAT	A	T	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment).	2.40E-57	

696	cg43153425	287	TGGGTTCTACTG AATCTCGGGTTG A/C/T/TACATGGG CTCAAGCATCCT CATGG	C	T	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment).	2.40E-57	
697	cg30384142	40	CTTGCGCGGCA CCAGGCGGTAA GAC[G/A]ACCCA TATTTAGAACT GGCACCTC	G	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P44788 SUN PROTEIN (FMU PROTEIN) - Haemophilus influenzae, 451 aa.	5.30E-56	
698	cg44015614	1289	GCTCTGGCTGG GGTGCAGTATAC TT[C/T]TCCACGT ATTCTATTTCCA CAACTT	C	T	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa.	3.30E-54	
699	cg44015614	1295	GCTGGGGTGCA GTATACCTCTCC AC[G/A]TATTCTA TTTCCACAACCT CTTCTG	G	A	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa.	3.30E-54	
700	cg44015614	1313	TCTCCACGTATT CTATTTCCACAA C/T/C/TCTTCTGA TGAGATGTTCTC CATT	T	C	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa.	3.30E-54	
701	cg44015614	1319	CGTATTCATTT CCACAACCTCTT C/T/C/GATGAGAT GTTCTCCATTTC CATGT	T	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa.	3.30E-54	

702	cg44015614	1325	CTATTTCCACAA CTTCTTCTGATG A/GA/ATGTTCTC CAATTCCATGTG TTTTGT	G	A	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa.	3.30E-54	
703	cg44015614	1379	AGGGCATTGCG AGAAACTGGCC CTT[A/G]ATAAGG AAATCAAACCTCC ACATGTT	A	G	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa.	3.30E-54	
704	cg42380652	406	AGTCCAGGCAG GGGCCACGTC CTC[T/C]CGGTA CACCTTTCCAG GAAGGGGC	T	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62739 RABIN3 - RATTUS NORVEGICUS (RAT), 460 aa.	4.20E-54	
705	cg43931038	425	TCTTCTCTAGAG TCCCGCGGCTC AC[A/G]GCCCTT GCTGCGAAGGG CAACTTGT	A	G	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa.	6.10E-54	11
706	cg43931038	436	GTCCCGCGGCT CACAGCCTTTGC TG[C/G]GAAGGG CAACTTGTTGGC AACCTGG	C	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa.	6.10E-54	11
707	cg43931038	463	AAGGGCAACTTG TGGGCAACCTG GT[C/T]AAGGAAA CCTTGACTTCTT CAAATT	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa.	6.10E-54	11

708	cg43931038	469	AAC TTG TGG GCA A ACCTGGTCAAG GAJA/CJACCTTGA CTTCTTCAAATT CACAAAC	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa.	6.10E-54	11
709	cg43931038	478	GCAACCTGGTCA T AGGAAACCTTGA CJT/CJTCTTCAAA TTCACAAAGCCCC ACCCA	C	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa.	6.10E-54	11
710	cg43931038	496	CCTTGACTTCTT C CAAATTCACAAC G[C/T]CCACCCA TCTCTACAACAA GGCGGC	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa.	6.10E-54	11
711	cg43931038	562	TCACGTAGTGGT G CAATAGCACCTT T[G/A]CCTCCCC CCATGCGATGC CCAACAC	A	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa.	6.10E-54	11
712	cg43338979	360	CATCATCTCCTG C AAGATGCTAGCA C[C/T]GTTCCTGT TATATCCAAC T CACTC	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O45933 Y43F4B.4 - CAENORHABDITIS ELEGANS, 363 aa.	1.40E-53	18
713	cg38450437	104	GAATTGGTTCTG G AGGAGTTTGAG GA[G/A]CTTCTTT TACTGATGGACA GAAATC	A	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43168 KIAA0443 - HOMO SAPIENS (HUMAN), 1395 aa.	3.50E-52	
714	cg38450437	47	CCAGGGAAGT T GCACAGCCAGA GAA[T/C]TGGTCT TGCAACTGCATC CAGTGTG	C	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43168 KIAA0443 - HOMO SAPIENS (HUMAN), 1395 aa.	3.50E-52	

715	cg43314946	458	CCTTCCGGATGAC CTTTCTCCGCAT C/C/T/TGCCCCA GCAGCTGGACA GCATACA	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD37447 BAW - FUGU RUBRIPES (JAPANESE PUFFERFISH) (TAKIFUGU RUBRIPES), 402 aa.	1.60E-51	17
716	cg44010070	320	TCAAGCACTCGG ACGGGACGCGC AC/T/C/TGCGCC AAGCTCTATGAC AAGAGCG	C	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O35775 SYNCOLLIN (SIP9) - Rattus norvegicus (Rat), 145 aa.	6.40E-51	
717	cg39380052	563	ACCTCATCACCC CGTACCATCAGA C/C/T/TCTCGACAA GGTCACTGAGC GTTTTTC	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB42016 PUTATIVE ADENYLOSUCCINATE SYNTHETASE - STREPTOMYCES COELICOLOR, 427 aa.	1.30E-50	
718	cg39380052	641	GTCGTGGCATC GGGCCGACCTA CTC/T/CjGACAA GATCAATCGGAT GGGTATTC	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB42016 PUTATIVE ADENYLOSUCCINATE SYNTHETASE - STREPTOMYCES COELICOLOR, 427 aa.	1.30E-50	
719	cg39380052	662	ACTCTGACAAGA TCAATCGGATGG G/T/CjATTTCGCGT CCAGGATCTTTT CGACG	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB42016 PUTATIVE ADENYLOSUCCINATE SYNTHETASE - STREPTOMYCES COELICOLOR, 427 aa.	1.30E-50	
720	cg43329819	585	TCATCGACAACC AGAACCTCCTCT T/T/CjGAGCTCTC CTACAAGCTGGA GGCAA	C	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92565 MYELOBLAST KIAA0277 - HOMO SAPIENS (HUMAN), 580 aa.	1.40E-50	
721	cg43298242	138	CTGAAGATCTGT TGGCAGGGCTC AC/A/GjGAGACG GGGGTGAGGGG AGAGATCG	A	Ser	Ser	SILENT- CODING	water_ch annel	Human Gene SWISSPROT- ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa.	1.30E-163	

722	cg43298242	150	TGGCAGGGCTC ACAGAGACGGG GGT[G/A]AGGGG AGAGATCGTGG GTTCATGAG	G	A	Leu	Leu	SILENT- CODING	water_ch annel	Human Gene SWISSPROT- ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa.	1.30E-163	
723	cg43970780	1501	GGAGTTCTGGTT CTGGTAGATGGA A[G/A]CTTTCTCT TTCAACAGGTCC AGACA	G	A	Ala	Val (1096)	CONSERVATI VE	apoptosi s	Human Gene SWISSNEW-ID:Q92785 ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIEM) - HOMO SAPIENS (HUMAN), 391 aa.[pcIs:SWISSPROT-ID:Q92785 ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIEM) - HOMO SAPIENS (HUMAN), 391 aa.	2.30E-212	11
724	cg43957906	460	GGAGTCCTTGG CGGCGTCATATG GGT[C]GCTCCT TGGAGGGGATC TCCAGGAC	T	C	His	Arg (1097)	CONSERVATI VE	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:Q16864 VACUOLAR ATP SYNTHASE SUBUNIT F (EC 3.6.1.34) (V-ATPASE F SUBUNIT) (V-ATPASE 14 KD SUBUNIT) - HOMO SAPIENS (HUMAN), 119 aa.	2.20E-58	12
725	cg43952088	2923	TGAGGGGAGCG TCGCCGGCCGC GGA[G/A]CAGAT GCCGCGGGGCG CGCTCGCAG	G	A	Ala	Val (1098)	CONSERVATI VE	cadherin	Human Gene SPTREMBL-ID:Q15065 OB-CADHERIN-1 - HOMO SAPIENS (HUMAN), 796 aa.	0.00E+00	16

726	cg4395666	613	ACTCCTGTTCTG GGGACAGTTTG GT[A/G]TTAAAC ACTTAAATATAG ATCCGG	A	G	Ile	Val (1099)	CONSERVATIVE	cadherin	Human Gene SWISSNEW-ID:Q08722 LEUKOCYTE SURFACE ANTIGEN CD47 PRECURSOR (ANTIGENIC SURFACE DETERMINANT PROTEIN OA3) (INTEGRIN ASSOCIATED PROTEIN) (IAP) (MER6) - HOMO SAPIENS (HUMAN), 323 aa.lpcis:SWISSPROT-ID:Q08722 LEUKOCYTE SURFACE ANTIGEN CD47 PRECURSOR (ANTIGENIC SURFACE DETERMINANT PROTEIN OA3) (INTEGRIN ASSOCIATED PROTEIN) (IAP) (MER6) - HOMO SAPIENS (HUMAN), 323 aa.	1.20E-167	3 (3q13.1)
727	cg43942011	1327	TTCCCCATGTGA AACATCTGGCTT G[C/T]GACAGGT GATTTTTCACA GGTAGG	C	T	Arg	His (1100)	CONSERVATIVE	complement receptor	Human Gene Similar to TREMBLNEW- ID:E246058 COMPLEMENT RECEPTOR 2 - MUS MUSCULUS (MOUSE), 651 aa (fragment).	1.10E-69	1 (1q32)
728	cg43973728	987	TATGAACCAACCC AGATCTGAAGAA G[T/C]TGCTGTTC TGAAACAGAAAGT TGGAG	T	C	Val	Ala (1101)	CONSERVATIVE	cyclin	Human Gene SWISSPROT- ID:P51946 CYCLIN H (MO15- ASSOCIATED PROTEIN) (P37) (P34) HOMO SAPIENS (HUMAN), 323 aa.	2.60E-172	5 (5q13.3)
729	cg44017721	291	TCCTGCTCCTCC GTGGCCTCCTTT G[G/A]CAGCGCT GGCCAAAGCCCC GGGTCAG	G	A	Ala	Val (1102)	CONSERVATIVE	cytochrome	Human Gene Similar to SPTREMBL- ID:O00761 CYTOCHROME OXIDASE SUBUNIT VIA HEART ISOFORM PRECURSOR (EC 1.9.3.1) (CYTOCHROME-C OXIDASE) (CYTOCHROME A(3)) (CYTOCHROME AA(3)) - HOMO SAPIENS (HUMAN), 97 aa.	2.40E-52	22

730	cg43273880	5428	CAAAAGAAGAAA GACGACGTGAC TG[G/C]GGGTAA GAAACCATTTG TCCAGAG	G	C	Gly	Ala (1103)	CONSERVATI VE	dna_rna_ bind	Human Gene SWISSPROT- ID:O14647 CHROMODOMAIN- HELICASE-DNA-BINDING PROTEIN 2 (CHD-2) - HOMO SAPIENS (HUMAN), 1739 aa.	0.00E+00	15
731	cg43992911	485	GAAGAAGAACTT TTTTAACTGAA C[A/G]ATAAAAGT GAAAAGATAAG AAGGA	A	G	Asn	Asp (1104)	CONSERVATI VE	glycoprot ein	Human Gene SWISSPROT- ID:P08183 MULTIDRUG RESISTANCE PROTEIN 1 (P- GLYCOPROTEIN 1) - HOMO SAPIENS (HUMAN), 1280 aa.	0.00E+00	7
732	cg41029366	890	TGCGGCCACAA AGAGGACGCGG GCG[T/C]GGTGT GCTCAGAGCAC CAGTCCTGG	T	C	Val	Ala (1105)	CONSERVATI VE	glycoprot ein	Human Gene SPTREMBL-ID:Q61003 T CELL SURFACE GLYCOPROTEIN CD6 - MUS MUSCULUS (MOUSE), 665 aa.	1.00E-234	11
733	cg43931167	2546	CGAGAACTGAA GAAAGCAAGAAC AG[T/G]CCTACAA ATGGATGAACTC AAATGT	T	G	Val	Gly (1106)	CONSERVATI VE	helicase	Human Gene SWISSPROT- ID:O14232 PUTATIVE HELICASE C6F12.16 IN CHROMOSOME I - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 1117 aa.	3.30E-307	5
734	cg43925670	2360	AATCTGAATTTT GTCATACTCTTC T[C/T]TCATTTTA AATTAAGTTTTAA ATC	C	T	Arg	Lys (1107)	CONSERVATI VE	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.[pcIs:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0.00E+00	1

735	cg43925670	2474	TAGAACAAATGTT CTTGATATTTTT [C/G]CCATCTTTA CAGACATAAGTG AGCC	C	G	Gly	Ala (1108)	CONSERVATI VE	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0.00E+00	1
736	cg43928549	4637	AATTGGCACATC TTGGCGCGAAA GT[C/T]GTTCAC TCTGGGTCGCA CAAGGAG	C	T	Asp	Asn (1109)	CONSERVATI VE	kinase	Human Gene SWISSNEW-ID:O00329 PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, DELTA ISOFORM (EC 2.7.1.137) (PI3- KINASE P110 SUBUNIT DELTA) (PTDINS-3-KINASE P110) (PI3K) (P110DELTA) - HOMO SAPIENS (HUMAN), 1044 aa.lpcis:SWISSPROT- ID:O00329 PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, DELTA ISOFORM (EC 2.7.1.137) (PI3- KINASE P110 SUBUNIT DELTA) (PTDINS-3-KINASE P110) (PI3K) (HUMAN), 1044 aa.lpcis:SPTREMBL- ID:O00329 PHOSPHOINOSITIDE 3- KINASE - HOMO SAPIENS (HUMAN), 1044 aa.	0.00E+00	
737	cg42703622	409	GAAGAAGGAATT TGGAGGTGGCC ACIA/GJTAAAGA TGAAGTATTTGG AACAGT	A	G	Ile	Val (1110)	CONSERVATI VE	kinase	Human Gene SPTREMBL-ID:Q12792 PROTEIN TYROSINE KINASE - HOMO SAPIENS (HUMAN), 350 aa.	3.00E-187	12

738	cg44131752	925	CTCTGCGTGCTC GTCCCGAAGTG AC[C/G]TGCCTG GTTCCGACAAG GACACTGA	G	Leu	Val (1111)	CONSERVATI VE	kinase	Human Gene SPTREMBL-ID:Q15599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA-1) - HOMO SAPIENS (HUMAN), 450 aa.	7.80E-173	16
739	cg25143358	394	CAGGTGGCCATT CGGGCGGCTTC AA[G/T]TTTCGTG GTCATGCCGCC GGTTCCC	T	Leu	Ile (1112)	CONSERVATI VE	kinase	Human Gene Similar to SWISSPROT- ID:P46546 GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK) - CORYNEBACTERIUM GLUTAMICUM, 369 aa.	2.70E-51	
740	cg43105476	702	GCGAAACCAAGTT CGGTCTTTCAAA TTC/TGGGATTAG CACCTCTAAGTA GCAGT	T	Asp	Asn (1113)	CONSERVATI VE	kinase inh ibitor	Human Gene Similar to SWISSPROT- ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa.	7.80E-86	
741	cg38642684	290	ATATTGCCTAGT AATTTCTGATAAT [C/T]ATTTAAGGT ATGTAAGTTGCT AGTA	T	Asp	Asn (1114)	CONSERVATI VE	nuclease	Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcis:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	2.60E-50	
742	cg39518465	864	CACCTCCTAAAG GAGATGAAGGA AG[C/T]CCTGGG CACCCCTGGCG CAGCCAAT	T	Ala	Val (1115)	CONSERVATI VE	oncogen e	Human Gene SWISSPROT- ID:P15498 VAV PROTO-ONCOGENE HOMO SAPIENS (HUMAN), 846 aa.	0.00E+00	

743	cg43021380	176	CAGCCGCCCGG GGGGCTGCAGC GCC[G/A]TTAGT GCCACGGCTG TCTATTTGA	G	A	Val	Ile (1116)	CONSERVATI VE	phosphat ase	Human Gene SWISSPROT- ID:Q16849 PROTEIN-TYROSINE PHOSPHATASE N PRECURSOR (EC 3.1.3.48) (R-PTP-N) (PTP IA-2) (ISLET CELL ANTIGEN 512) (ICA 512) (ISLET CELL AUTOANTIGEN 3) - HOMO SAPIENS (HUMAN), 979 aa.	0.00E+00	2
744	cg39728924	365	CAATTGTGGAGA AGAGTATTTTAT [G/A]TCGCTACTC AAGACCACTG CTGAG	G	A	Val	Ile (1117)	CONSERVATI VE	phosphat ase	Human Gene Similar to TREMBLNEW- ID:D1024666 PROTEIN-TYROSINE- PHOSPHATASE (EC 3.1.3.48) - MUS MUSCULUS (MOUSE), 426 aa.	1.20E-64	
745	cg42710490	851	CAACCAGCCTAT TGGGGGAAGAA AT[G/A]TCCAGG GTGGAATCCGTT TTGGGGA	G	A	Val	Ile (1118)	CONSERVATI VE	polymera se	Human Gene SWISSNEW-ID:O54888 DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT) - RATTUS NORVEGICUS (RAT), 1135 aa. pcis: TREMBLNEW-ID:G2739048 RNA POLYMERASE I 127 KDA SUBUNIT - RATTUS NORVEGICUS (RAT), 1135 aa.	8.90E-172	
746	cg44001078	316	GGTTATCAGGAA CTTGGGATCTTC A[C/T]GGATTTC ATCTTGTTCTTC ATCCA	C	T	Arg	His (1119)	CONSERVATI VE	struct	Human Gene TREMBLNEW- ID:G2920823 CARDIAC MYOSIN BINDING PROTEIN-C - HOMO SAPIENS (HUMAN), 1274 aa.	0.00E+00	
747	cg43916919	1113	AGGTAGGAGTC CCCCGAGAAGA AGA[C/T]GCCCT GGTTCTCTTGCG CCACAGGC	C	T	Val	Ile (1120)	CONSERVATI VE	struct	Human Gene SWISSNEW-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP-G) - HOMO SAPIENS (HUMAN), 348 aa. pcis: SWISSPROT-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP-G) - HOMO SAPIENS (HUMAN), 348 aa.	4.3E-188	2 (2cen)

748	cg42930605	463	CAGCTCCTTGCT GGTCTTCTGCAC C[C]/TTCACCTCC ATGTCGTACTTC TCCTC	C	T	Arg	Lys (1121)	CONSERVATI VE	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)
749	cg36824552	230	AAGACGAGCCG AGGCTTCACCTA CC[A]/GJCCTGCA CTTCTGGCTCGG AAAGGAG	A	G	His	Arg (1122)	CONSERVATI VE	struct	Human Gene Similar to SWISSPROT- ID:Q28046 ADSEVERIN (SCINDERIN) (SC) - BOS TAURUS (BOVINE), 715 aa.	4E-80	
750	cg42522566	377	CAACATCATGAA CCAGCTCAGCC AC[G]/ATAAACTT GATCCAACTTTA TGATGC	G	A	Val	Ile (1123)	CONSERVATI VE	struct	Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa.	6E-55	
751	cg42522566	509	GTACCACCTCAC TGAGTTGGATGT G[G]/ATCTTGTTG ACGAGGCAGAT CTGTGA	G	A	Val	Ile (1124)	CONSERVATI VE	struct	Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa.	6E-55	
752	cg42489842	481	TGCAAGTGAATA TGCCAAATACTG C[T]/A/CAGAAATA TTAGGAGTTGCA GCTAC	T	A	Ser	Thr (1125)	CONSERVATI VE	tm7	Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS SCROFA (PIG), 704 aa.	7.3E-106	
753	cg43919398	2201	GTTAGTCTCTGT GGTGTGCTTATA A[T]/C/CATTGGG GTCCAAACATTCA CATT	T	C	Ile	Val (1126)	CONSERVATI VE	transcript factor	Human Gene SWISSPROT- ID:Q14188 TRANSCRIPTION FACTOR DP-2 (E2F DIMERIZATION PARTNER 2) - HOMO SAPIENS (HUMAN), 385 aa.	2.7E-202	3

754	cg20612302	300	ATGAGGCGGC CCACATGGCGG CCA[C/G]CGCCA TCCTCAACCTGT CCACGCGC	C	G	Thr	Ser (1127)	CONSERVATI VE	transcript factor	Human Gene Similar to SPTREMBL- ID:O08996 MYELIN TRANSCRIPTION FACTOR 1-LIKE - MUS MUSCULUS (MOUSE), 1182 aa.	1.7E-53	
755	cg44928196	1474	GGCTCTGTTCCA TGGGAAATTCAT A[G/A]ACACGGG TTTTCTTTACCA TTCTA	G	A	Asp	Asn (1128)	CONSERVATI VE	ubiquitin	Human Gene TREMBLNEW- ID:G2827198 UBIQUITIN PROTEIN LIGASE - MUS MUSCULUS (MOUSE), 854 aa.	0	
756	cg43301812	3784	GGCTGGTCTCTT TCCATGGCTGG GAT/CJGCTCTG CTGCGCTTGGTT TTGCCCG	T	C	His	Arg (1129)	CONSERVATI VE	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q93075 HYPOTHETICAL PROTEIN KIAA0218 - Homo sapiens (Human), 761 aa.	0.00E+00	3
757	cg43917191	2735	GCTTCTCTTTTC ACATTGTATGTA T[C/T]CAGGTGTT CTTGCAACTCCA AAACA	C	T	Asp	Asn (1130)	CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74849 KIAA0826 PROTEIN - HOMO SAPIENS (HUMAN), 1236 aa (fragment).	0.00E+00	4
758	cg43918356	2637	GCTCATGTCATC TTCATCTAGAAA C[G/A]CCCTCAC GGAAATGGAATT GCTGCC	G	A	Ala	Val (1131)	CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75176 KIAA0892 PROTEIN - HOMO SAPIENS (HUMAN), 783 aa (fragment).	0.00E+00	12
759	cg43932090	1186	TCCTTTCAAGCT TTCCTTATGTTGT T[C/T]ATTGTCTT CATTTCTTGAA GGTC	T	C	Lys	Arg (1132)	CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O00566 M PHASE PHOSPHOPROTEIN 10 - HOMO SAPIENS (HUMAN), 672 aa (fragment).	0.00E+00	
760	cg43950437	794	AGCCAGAGGCT GGTACCTAGAAC CA[G/C]TGGATG GTTCTTGGCTG ATGGCGC	G	C	Thr	Ser (1133)	CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q15021 ORF - HOMO SAPIENS (HUMAN), 1401 aa.	0.00E+00	12

761	cg42935995	743	GCCTCGCTCCC CGTCTGAGAGC CTC[A/G]CGCCC TCCAGCCAGCC GTCACGTCT	A	G	Val	Ala (1134)	CONSERVATI VE	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q12774 PROBABLE GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM (ONCOGENE TIM) (P60 TIM) (TRANSFORMING IMMORTALIZED MAMMARY ONCOGENE) - Homo sapiens (Human), 519 aa.	1.00E-274	
762	cg43971614	2578	TCCATTTGAATC CAATCCCCCATG G[A/G]CATAAGA AGAGTTCTTTCC ATAAAA	A	G	Val	Ala (1135)	CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13283 GAP SH3 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 466 aa.	5.30E-253	5
763	cg43922856	1581	CTTGAAATTTC AGTCACCCCTATT G[A/G]CAACTAA GGATTCGTTGCT TGAAGC	A	G	Val	Ala (1136)	CONSERVATI VE	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa.	2.00E-237	12 (12q22)
764	cg43922856	1783	CCACTTGTCAT TCAGTCTCAGTT ATT/CITCCAGCTT GAGAAATAGCTCT GATTG	T	C	Ile	Val (1137)	CONSERVATI VE	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa.	2.00E-237	12 (12q22)
765	cg43955639	282	GGCCGCGGGG GATAGCTGCCCA GG[C/G]TCAGGA GGCTCTTGGGCT CCTGCCA	C	G	Ser	Thr (1138)	CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O15417 CAGL79 - HOMO SAPIENS (HUMAN), 413 aa (fragment).	2.80E-215	
766	cg41022625	1121	CACGGGTTTCT GGATCGTCTTCT CC[A/G]TCATTCA CATCATGCCAC CCTGCT	A	G	Ile	Val (1139)	CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34036 CGI-40 PROTEIN - HOMO SAPIENS (HUMAN), 845 aa.	2.00E-207	11

767	cg43119894	1960	TGAGCATAGCTC TGAGCTCTCTTT A/C/TACGGTCA GGTCCACATAA TGCATT	C	T	Val	Ile (1140)	CONSERVATIVE	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAA75235 LACTOSYL CERAMIDE ALPHA-2,3-SIALYLTRANSFERASE (EC 2.4.99.9) MUS MUSCULUS (MOUSE), 387 aa.	2.30E-190	2
768	cg43303845	1109	AGAACGAGAGA GGCTGGAGAGA CTG/C/GAACGG GAGAGGCAAGA AAGGGAGCG	C	G	Gln	Glu (1141)	CONSERVATIVE	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O93263 AVENA - GALLUS GALLUS (CHICKEN), 550 aa.	1.90E-138	
769	cg44927166	531	GTCCTTGTCTTC CCAATCCCTTTG G/C/TJGTCTCGT TCTTTATCCCTTT CTCT	C	T	Arg	His (1142)	CONSERVATIVE	UNCLASSIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA74876 KIAA0853 PROTEIN - HOMO SAPIENS (HUMAN), 967 aa (fragment).	3.70E-133	13
770	cg38059286	473	AGCTGTATAGCT CCAGTGGTCCCT GA[G/T]CTCCGC CGCTCCCTCTTC TCACTGA	G	T	Glu	Asp (1143)	CONSERVATIVE	UNCLASSIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD39906 FH1/FH2 DOMAIN-CONTAINING PROTEIN FHOS - HOMO SAPIENS (HUMAN), 1164 aa.	4.00E-129	
771	cg29351416	333	CTGCCAGCCA GCCCCATCCCCCT GA[G/T]GACCTG GCTTTGTCAATG GGCACCA	G	T	Glu	Asp (1144)	CONSERVATIVE	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1-INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1-INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa.	3.20E-127	
772	cg43960639	987	CCATGCTGGGA GAATGGGAGCC TC[A/C]TCGCC ACTTGAAAGTCA AAGTAGA	A	C	Asp	Glu (1145)	CONSERVATIVE	UNCLASSIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB40416 P24B PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 217 aa.	9.00E-111	

773	cg43325007	1098	GTGGATATATGT GGCCTGCAGTAT G[G/A]CCCACAG CTTCTCCTGGAG GCTGCC	G	A	Ala	Val (1146)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD43195 PEROXISOMAL MEMBRANE PROTEIN PMP 24 - HOMO SAPIENS (HUMAN), 212 aa.	4.80E-110	20
774	cg42907145	853	GCCACCTCCCAT AACCTTCTCAGC A[G/A]CATAGACT GACTTGCCACAT CGAGG	G	A	Ala	Val (1147)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50461 LIM DOMAIN PROTEIN, CARDIAC (MUSCLE LIM PROTEIN) (CYSTEINE- RICH PROTEIN 3) (CRP3) (LIM-ONLY PROTEIN 4) - Homo sapiens (Human), 194 aa.	1.10E-108	11
775	cg43972159	1374	AAGCCATTAGGT TCTCGGGCTGCT G[A/T]ACTGTTCCG ATTTTGACTTTTC TTTC	A	T	Ser	Thr (1148)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa.	2.60E-102	7 (12q24.1)
776	cg39512856	508	CCAGGCTGTGC CGTCCACTTCT GAT[A/T]ATCCCC TCCCGGCGATAA CCAGGT	T	A	Tyr	Phe (1149)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	
777	cg28461713	584	TCTGCAAAATTG CTCCTGGGCAT GG[G/A]CAGCTT GCAGCTGAAGTT GGTTGTA	G	A	Ala	Val (1150)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47710 ALPHA-S1 CASEIN PRECURSOR - Homo sapiens (Human), 185 aa.	5.90E-96	4 (4q21.1)
778	cg43969092	361	CGGCGCCCGTC ATCACGGATGTG CA[C/A]GTCCCC GTCGGTCAGCA GCAGCACA	C	A	Val	Leu (1151)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA74913 KIAA0890 PROTEIN - HOMO SAPIENS (HUMAN), 1194 aa.	6.30E-89	

779	cg42688841	487	GCGTCATAGTAT AAAGAAAGGCTTG A/C/TGACAAACA GTCTCTTGCCAT GGTCC	C	T	Val	Ile (1152)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (Cl- SGDH) - Bos taurus (Bovine), 189 aa.	1.90E-83	
780	cg39523553	603	GACGCGTTGGTT CCCGACGAAGA CG/C/TJCCGAGC GGCCAAGTGGG CGGTGGCG	C	T	Ala	Val (1153)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.20E-75	
781	cg39523553	819	ATGGACGTGGT GCGCAACAGCC CTC/A/GICGGAG TGAAGGTCAG TGGCTCTT	A	G	His	Arg (1154)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.20E-75	
782	cg39523553	857	CCAGATGGCTCT TTCCGCCTGGC CC/G/CJAGCTCG ATCAGGCATCAA GGTGCCT	G	C	Glu	Gln (1155)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.20E-75	
783	cg35933325	274	AACCACAGAGAA TACAGTGACAAC A/A/TJAGAAACAA AATGACCAAATG CCACT	A	T	Phe	Tyr (1156)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA74845 KIAA0822 PROTEIN - HOMO SAPIENS (HUMAN), 1581 aa.	2.40E-74	
784	cg41677120	544	GTTGTTTAACCT AAGCAATTTTT G/G/AJATAAAAGT GGATTGCAAGG ATATGA	G	A	Asp	Asn (1157)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	1.10E-71	11
785	cg43951096	2850	AACATCAACAAT CGTTATTGGGTC TTT/CJTATTTTTG CTAGAAGAAGTA TCTGG	T	C	Lys	Arg (1158)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa.	2.00E-71	17

786	cg42696021	444	GCTGTGCCGCC TTCACAATGAAG TGIA/GIACCGGA AGCTGGGCAAG CCTGATTT	A	G	Asn (1159)	Asp (1159)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
787	cg34243633	447	GCTGGCACCGA CATAAGAACTTG TTT/CJTCCAGCT GGGAGCAGCA TGGCAAC	T	C	Lys (1160)	Arg (1160)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa.	1.30E-68	
788	cg34243633	472	TTCCAGCTGGG GAGCAGCATGG CAAIC/TJCAGTGT GCCCAAAAGCC CCAGAAGG	C	T	Val (1161)	Ile (1161)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa.	1.30E-68	
789	cg43942922	268	GTCCTCTGTCAA GACCCCTGAAAC A[G/A]TTGTCCCC ACAGCCCCTGA GCTCCA	G	A	Val (1162)	Ile (1162)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.30E-68	
790	cg43942922	310	TGAGCTCCAGC CTTCCACCTCCA CA[G/A]ACCAGC CTGTCACCTCTG AGCCAC	G	A	Asp (1163)	Asn (1163)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.30E-68	
791	cg44938009	1139	TTCTGTCAATGT GGTCCGTGCCA TGIA/GJTTGATAA CTGGGATGTCCT CTTCCA	A	G	Ile (1164)	Val (1164)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SWISSNEW-ACC:O43182 RHO-GTPASE-ACTIVATING PROTEIN 6 (RHO-TYPE GTPASE-ACTIVATING PROTEIN RHO GAPX-1) - Homo sapiens (Human), 587 aa.	5.80E-66	X

792	cg39516123	631	AGCCCTCAGGC GCGCCACAGAA CAGT/GJGGGCA CCAACACTCCCC CTAGTCCT	T	G	Val	Gly (1165)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa.	5.10E-62	
793	cg44921974	279	GATTATGTCGCC GTTGAGTTCGGT C/A/GJCAGACTT GATGTTTTTGAA AGTTGT	A	G	Val	Ala (1166)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P07148 FATTY ACID-BINDING PROTEIN, LIVER (L-FABP) - Homo sapiens (Human), 127 aa.	1.6E-61	2 (4q28)
794	cg42731307	497	AAGGCATTGATG ATCCGGTCCCC CA/G/CJTGGGT GATGGCAAGTTC TGAATC	G	C	Leu	Val (1167)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa.	2.60E-61	
795	cg42731307	534	CAAGTCTGGAA TCCTCTGGAAT C/T/GJTCCCGGC TGAGAGTCCCAT TCTCTC	T	G	Glu	Asp (1168)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa.	2.60E-61	
796	cg44015614	1330	TCCACAACCTTCT TCTGATGAGATG T/T/CJCTCCATT CCATGTGTTTGT CCAAG	T	C	Asn	Asp (1169)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa.	3.30E-54	
797	cg43298242	143	GATCTGTTGGCA GGGCTCACAGA GA/C/TJGGGGGT GAGGGGAGAGA TCGTGGGT	C	T	Val	Ile (1170)	CONSERVATI VE	water_ch annel	Human Gene SWISSPROT- ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa.	1.3E-163	

798	cg43299510	842	CTCCAGTGCC CGCCCGACTAC CACCTTACATCC ACACCGAGATCT CCCGGA	C	T	His	Tyr (1171)	NON- CONSERVATI VE	ATPase_ associated	Human Gene Homologous to SWISSPROT-ID:P39986 PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38) - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1215 aa.	1.40E-109	
799	cg42532480	564	TTTCCTGAATGA ATGTTAAAGATT CTT/AGTCAAGGT CAGTATGGCGAT CCAAG	T	A	Arg	End (1172)	NON- CONSERVATI VE	cadherin	Human Gene Homologous to SWISSPROT-ID:P79995 CADHERIN- 10 PRECURSOR - GALLUS GALLUS (CHICKEN), 789 aa. pcis:SPTREMBL- ID:P79995 CADHERIN-10 - GALLUS GALLUS (CHICKEN), 789 aa.	6.00E-115	
800	cg42926989	259	GCAATGAGCTG CTGGCAGCACA AAG/GTCTTATC GCACCAGGAAA GATGCAGC	G	T	Ala	Asp (1173)	NON- CONSERVATI VE	cathepsi n	Human Gene Homologous to SWISSPROT-ID:P08311 CATHEPSIN G PRECURSOR (EC 3.4.21.20) - HOMO SAPIENS (HUMAN), 255 aa.	1.7E-136	14 (14q11.2)
801	cg43991318	2521	TGGTCCGGGAA TACCTGGTGGAC CCIT/GJCGGGC CCGGCTGCCAG GAGCTGCC	T	G	Cys	Gly (1174)	NON- CONSERVATI VE	collagen	Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa.	1.3E-73	1 (1p34)
802	cg43920512	1467	AATTCAAAGTAT CATGGTGTCTTCT CTT/CJCTCAACC CACCAGAGACA CTAAAT	T	C	Leu	Pro (1175)	NON- CONSERVATI VE	cyclin	Human Gene SWISSPROT- ID:P20248 G2MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa.	4.1E-231	4 (4q27)
803	cg43063374	1763	AGAGATTGAACGA TGTTGGTGGCAG A[A/C]ACCGGAG CCCCTGCATGCA GGACAG	A	C	Asn	His (1176)	NON- CONSERVATI VE	cyto450	Human Gene SWISSNEW-ID:P33259 CYTOCHROME P450 2C17 (EC 1.14.14.1) (CYPIIC17) (P450-254C) - HOMO SAPIENS (HUMAN), 468 aa. pcis:SWISSPROT-ID:P33259 CYTOCHROME P450 IIC17 (EC 1.14.14.1) (P450-254C) - HOMO SAPIENS (HUMAN), 468 aa.	3.2E-254	10 (10q24.1)

804	cg21416244	360	GGGTGAACGTG CTATCCACCAT ATC/TATCTATT CAGGCACATTCA GGACCT	C	T	Ser	Leu (1177)	NON- CONSERVATI VE	cytochrome	Human Gene Similar to SWISSPROT- ID:P98001 CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) - SACCCHAROMYCES DOUGLASII (YEAST), 534 aa.	5.5E-69	
805	cg44017721	217	AGATAGGAGTTG AAGGTGCAGAG GG[C/T]CAGCT GGGCAGCGCCA GCACGAAG	C	T	Ala	Thr (1178)	NON- CONSERVATI VE	cytochrome	Human Gene Similar to SPTREMBL- ID:O00761 CYTOCHROME OXIDASE SUBUNIT VIA HEART ISOFORM PRECURSOR (EC 1.9.3.1) (CYTOCHROME-C OXIDASE) (CYTOCHROME A(3)) (CYTOCHROME AA(3)) - HOMO SAPIENS (HUMAN), 97 aa.	2.4E-52	22
806	cg43275625	1105	TGGTACTCCTTT GCCGCCAGCTT GG[A/G]CTCATG GTACACGTTGG GTTTGGTA	A	G	Ser	Pro (1179)	NON- CONSERVATI VE	deaminase	Human Gene SPTREMBL-ID:O00465 DSRNA ADENOSINE DEAMINASE DRADA2C - HOMO SAPIENS (HUMAN), 714 aa.	0	21
807	cg43312829	1402	TAGTGAAAATCT CCAATCAAAGAC A[A/G]CAGGACT CCATGTAAGTGA ATAATGA	A	G	Thr	Ala (1180)	NON- CONSERVATI VE	dehydrogenase	Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 617 aa.	0	4

808	cg43959136	1144	TGGGCCAACAA GCTTGAGTGCG ATC C/TGGTCTG CAATGATGGAG GAATTGCC	C	T	Arg	Gln (1181)	NON- CONSERVATI VE	dehydrog enase	Human Gene SWISSNEW-ID:P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1-THF SYNTHASE) (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) - HOMO SAPIENS (HUMAN), 934 aa. pcis:SWISSPROT-ID:P11586 C-1- TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) (C1-THF SYNTHASE) - HOMO SAPIENS (HUMAN), 934 aa.	0	14
809	cg43969759	648	TGTCAGGAGGA AGATCTCATCTG GG A/G GTGCC GGATCCCGCGG GCGATGAC	A	G	Ile	Thr (1182)	NON- CONSERVATI VE	dehydrog enase	Human Gene Homologous to SPTREMBL-ID:Q16797 NADP- DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE) - HOMO SAPIENS (HUMAN), 572 aa.	1.8E-109	11

810	cg39523614	697	GGGAGCTTTAGAT CATTGCCACGGA TTT/CJACGTCCAG AAGCGCAAGCA GTTTGG	T	C	Tyr	His (1183)	NON- CONSERVATI VE	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) - MYCOBACTERIUM LEPRAE, 389 aa.	2.10E-76	
811	cg42175288	1152	TGGAGACCCCA AAAGTGGGATT GG[G/T]TTTGCC CTAATCCGTCAT GCGGAAA	G	T	Val	Phe (1184)	NON- CONSERVATI VE	dna_rna_ bind	Human Gene SPTREMBL-ID:Q92804 PUTATIVE RNA BINDING PROTEIN RBP56 - HOMO SAPIENS (HUMAN), 592 aa.	0.00E+00	17
812	cg43154217	1352	GCAGAAGAGGT GATTGTGAGAG GAC[C/A]AAGAG CTCCAGGGAACA GCTGGAACT	C	A	Gly	Cys (1185)	NON- CONSERVATI VE	dna_rna_ bind	Human Gene Similar to SWISSPROT- ID:P26599 POLYPYRIMIDINE TRACT- BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I) (57 KD RNA-BINDING PROTEIN PPTB-1) - HOMO SAPIENS (HUMAN), 531 aa.	2.20E-90	
813	cg39709402	108	GGAAACATTAA TAAACAAGTAGA A[G/C]CCTACAG AGAGGAATCGC AAAAATC	G	C	Ala	Pro (1186)	NON- CONSERVATI VE	dna_rna_ bind	Human Gene Similar to SPTREMBL- ID:O08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGICUS (RAT), 362 aa (fragment).	3.20E-57	
814	cg39709402	133	GCCTACAGAGA GGAATCGCAAAA AT[C/G]CCTGAAA GAATTCAGGAA AACACA	C	G	Ser	Cys (1187)	NON- CONSERVATI VE	dna_rna_ bind	Human Gene Similar to SPTREMBL- ID:O08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGICUS (RAT), 362 aa (fragment).	3.20E-57	
815	cg39709402	57	GATGCTGGAGG ACTTCAAGAAAG AC[A/G]TGAAGA ACTCCCTTAGAG AAACACA	A	G	Met	Val (1188)	NON- CONSERVATI VE	dna_rna_ bind	Human Gene Similar to SPTREMBL- ID:O08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGICUS (RAT), 362 aa (fragment).	3.20E-57	

816	cg39709402	76	AAAGACATGAAG AACTCCCTTAGA G/A/GAACACAG GAAACATTAA AAACAA	A	G	Glu (1189)	NON- CONSERVATI VE	dna_rna_ bind	Human Gene Similar to SPTREMBL- ID:O08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGICUS (RAT), 362 aa (fragment).	3.20E-57	
817	cg39709402	94	CTTAGAGAAACA CAGGAAAACATT A/A/GJTAACAAG TAGAAGCCTACA GAGAG	A	G	Ser (1190)	NON- CONSERVATI VE	dna_rna_ bind	Human Gene Similar to SPTREMBL- ID:O08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGICUS (RAT), 362 aa (fragment).	3.20E-57	
818	cg39709402	96	TAGAGAAACACA GGAAAACATTAA T/A/GJAAACAAGTA GAAGCCTACAGA GAGGA	A	G	Glu (1191)	NON- CONSERVATI VE	dna_rna_ bind	Human Gene Similar to SPTREMBL- ID:O08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGICUS (RAT), 362 aa (fragment).	3.20E-57	
819	cg43950268	1949	TTTGCTATGTCC TCCTTGACCTCC T/G/AJCTCGGTG GCGGTCACAAT GCCCTCC	G	A	End (1192)	NON- CONSERVATI VE	eph	Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa.	0.00E+00	16
820	cg43985169	540	AAGACGAATGG GTGGTGGTAGA GAT/T/CJCTGAAG AAATGGAAATAG ATGGTGA	T	C	Pro (1193)	NON- CONSERVATI VE	eph	Human Gene Homologous to SWISSPROT-ID:P25685 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa.	2.40E-123	
821	cg43997616	2250	AAAGCCAGCGG AGCCGTAAGCAT CA/T/CJACTGCTT CCTCTTCACCTC ATCACT	T	C	Cys (1194)	NON- CONSERVATI VE	eph	Human Gene Similar to TREMBLNEW- ID:G2735762 HEAT SHOCK PROTEIN DNAJ - LEPTOSPIRA INTERROGANS, 369 aa.	1.40E-55	

822	cg43319420	992	CACGACAACTAC AGAAACAACCCC TTT/CJCCACAAC TCCGGCACTGCT TCTGC	T	C	Phe	Ser (1195)	NON- CONSERVATI VE	esterase	Human Gene Similar to SWISSNEW- ID:Q23917 3',5'-CYCLIC- NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa. pcis:SWISSPROT-ID:Q23917 3',5'- CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa.	3.30E-60	21
823	cg44034764	382	GAGGTCCAGGC TGGGCAGGACA GTCIT/CJCCCCAT GGTGCCGTAAAC AGCCTCTT	T	C	Glu	Gly (1196)	NON- CONSERVATI VE	glycoprot ein	Human Gene SWISSPROT- ID:P23276 KELL BLOOD GROUP GLYCOPROTEIN (EC 3.4.24.-) - HOMO SAPIENS (HUMAN), 732 aa.	0.00E+00	7 (Xp21.2)
824	cg43991224	217	TCTCATCTGTCT ACCTACAGCCTGG GTT/AJTGGGTCA TGGCAGCAGTG GTGCTG	T	A	Val	Asp (1197)	NON- CONSERVATI VE	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P41217 OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 274 aa (fragment).	1.50E-139	
825	cg44018623	1824	TACCATCTCTGT TTTTACCACTGG TIG/AJGCTCTGAA CAACAAATAATT TGTGG	G	A	Pro	Leu (1198)	NON- CONSERVATI VE	glycoprot ein	Human Gene Homologous to SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	1.90E-114	6
826	cg38924741	598	AAAGAGGAGAAT GGTGACTTTGCC TTT/CJATTCAGAG TGAACGAGCT GAAAGG	T	C	Leu	Ser (1199)	NON- CONSERVATI VE	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P04196 HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-PROLINE RICH GLYCOPROTEIN) (HPRG) - HOMO SAPIENS (HUMAN), 525 aa.	3.30E-55	

827	cg43322513	13082	TTCTGTTCTTC ACATGGTGAGC CC/C/TGGCCCTG CTGCTGCTTGC ATTCGGG	C	T	Arg	Gln (1200)	NON- CONSERVATI VE	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE- RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.30E-54	12
828	cg44913214	2306	GAACACAACAAA GAAAAAACAGAG T/C/TJTGGACTC ATCCAAAAGGGA CGAGA	C	T	Ser	Phe (1201)	NON- CONSERVATI VE	helicase	Human Gene TREMBLNEW- ID:G2801555 PUTATIVE ATP- DEPENDENT MITOCHONDRIAL RNA HELICASE - HOMO SAPIENS (HUMAN), 786 aa.	0.00E+00	10
829	cg39529972	278	TGGCCTCGACA TCATTCCCTGAC G/A/GJGGACTTA AAGGGTAGCAAT TCGTAT	A	G	Ser	Pro (1202)	NON- CONSERVATI VE	hydrolas e	Human Gene Similar to SWISSPROT- ID:Q01477 UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 3 (EC 3.1.2.15) (UBIQUITIN- THIOLESTERASE 3) (UBIQUITIN- SPECIFIC PROCESSING PROTEASE 3) (DEUBIQUITINATING ENZYME 3) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 912 aa.	1.00E-52	
830	cg43925670	2309	TAGTTTGCCCAA ACCAGCATCACC T/C/GJGGAACITTT TCCTCCATCAAG TCAGC	C	G	Arg	Pro (1203)	NON- CONSERVATI VE	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. lpcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0.00E+00	1

831	cg43925670	2369	TTTGTCATACTC TTCTCTCATTTT [A/G]AATTAAGTT TTAAATCGTTGC TCAG	A	G	Leu	Ser (1204)	NON- CONSERVATI VE	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0.00E+00	1
832	cg43925670	2458	CCTCTAATCCTT TTAGTAGAACAA T[G/T]TCTTGTA TTTTTTCCCATC TTTA	G	T	Asn	Lys (1205)	NON- CONSERVATI VE	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0.00E+00	1
833	cg43925670	2467	CTTTTAGTAGAA CAATGTTCTTGT A[T/G]TTTTTTCC CATCTTTACAGA CATAA	T	G	Lys	Asn (1206)	NON- CONSERVATI VE	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0.00E+00	1

834	cg43331742	845	TCCTCGAGGTG CTTCCCACAGAC TCG/AJATTCTG AGTTTCCACAG AAAAGA	G	A	Ser	Leu (1207)	NON- CONSERVATIVE	isomerase	Human Gene Homologous to SWISSPROT-ID:P70473 2- ARYLPROPIONYL-COA EPIMERASE (EC 5.---) - RATTUS NORVEGICUS (RAT), 361 aa.	5.60E-131	
835	cg43253796	1812	GAAATGGATCTT ATTTGGACTTTG CIG/TJACAAGACT GCCGAGAGATTT TCCCA	G	T	Arg	Leu (1208)	NON- CONSERVATIVE	kinase	Human Gene SWISSNEW-ID:P42338 PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, BETA ISOFORM (EC 2.7.1.137) (PI3- KINASE P110 SUBUNIT BETA) (PTDINS-3-KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1070 aa.lpcis:SWISSPROT-ID:P42338 PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, BETA ISOFORM (EC 2.7.1.137) (PI3- KINASE P110 SUBUNIT BETA) (PTDINS-3-KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1070 aa.	0.00E+00	
836	cg43257400	2094	GACATCAGCATG GCTGCCCCCGA CTT/CJCAGCAG AACATGATCATT CTCTGAC	T	C	Ser	Pro (1209)	NON- CONSERVATIVE	kinase	Human Gene SPTREMBL-ID:Q60680 CONSERVED HELIX-LOOP-HELIX UBIQUITOUS KINASE - MUS MUSCULUS (MOUSE), 745 aa.	0.00E+00	10
837	cg43974480	686	TCACGGACTTTG GACTGTCCAAA TIG/TGGCCTCAT GAGCCTGACAA CGAACT	G	T	Met	Ile (1210)	NON- CONSERVATIVE	kinase	Human Gene SPTREMBL-ID:O00114 HYPOTHETICAL HUMAN SERINE- THREONINE PROTEIN KINASE R31240_1 - HOMO SAPIENS (HUMAN), 1237 aa (fragment).	0.00E+00	

838	cg43922705	4337	CAAACCGGCTTT CTCCATGGTGCC CT/CJGCCAAAC CCTGGAGTTCCC AGGCTG	T	C	Gln	Arg (1211)	NON- CONSERVATI VE	kinase	Human Gene SWISSPROT- ID:P27987 ID-MYO-INOSITOL- TRISPHOSPHATE 3-KINASE B (EC 2.7.1.127) (INOSITOL 1,4,5- TRISPHOSPHATE 3-KINASE) (IP3K) (HOMO SAPIENS (HUMAN), 505 aa (fragment).	3.80E-279	1 (1q41)
839	cg38438124	1460	TGCAAAAACGTGT TAAACATGGCGC T[G/C]GCGCGGA GATCTCCACCGT GAACCC	G	C	Gly	Arg (1212)	NON- CONSERVATI VE	kinase	Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KII- ALPHA) (1- PHOSPHATIDYLINOSITOL-4- PHOSPHATE KINASE) (PTDINS(4)P- 5-KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS MUSCULUS (MOUSE), 405 aa.	2.80E-216	10
840	cg42703622	385	GTATGCAGCAAC AAGAGCAACTCT G[A/G]AGAAAGGA ATTGGAGGTGG CCACAT	A	G	Lys	Glu (1213)	NON- CONSERVATI VE	kinase	Human Gene SPTREMBL-ID:Q12792 PROTEIN TYROSINE KINASE - HOMO SAPIENS (HUMAN), 350 aa.	3.00E-187	12
841	cg42703622	395	ACAAGAGCAACT T CTGAAGAAGGAA TTT/CJTGGAGGT GGCCACATTAA GATGAA	T	C	Phe	Ser (1214)	NON- CONSERVATI VE	kinase	Human Gene SPTREMBL-ID:Q12792 PROTEIN TYROSINE KINASE - HOMO SAPIENS (HUMAN), 350 aa.	3.00E-187	12
842	cg41501665	96	GAGTACACCATC G AAGTCGCACTCC A[G/A]CTTGCCG CCCAACAACAGC TACGCC	G	A	Ser	Asn (1215)	NON- CONSERVATI VE	kinase	Human Gene Similar to TREMBLNEW- ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa.	2.70E-76	

843	cg25143358	457	GCTTTATGGTA TCGACATCCAAT GTC/TGTGGATG TCCTCCACAACC TCCACG	C	T	Ala	Thr (1216)	NON- CONSERVATI VE	kinase	Human Gene Similar to SWISSPROT- ID:P46546 GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK) - CORYNEBACTERIUM GLUTAMICUM, 369 aa.	2.70E-51	
844	cg29023997	179	TGCATGGTTCC ATTTCAATCTG GTA/GTGGGATG GAGCACCATGT GCGCACC	A	G	Asp	Gly (1217)	NON- CONSERVATI VE	kinasere ceptor	Human Gene SWISSPROT- ID:P36896 SERINE/THREONINE- PROTEIN KINASE RECEPTOR R2 PRECURSOR (EC 2.7.1.37) (SKR2) (ACTIVIN RECEPTOR-LIKE KINASE 4) (ALK-4) (ACTR-IB) - HOMO SAPIENS (HUMAN), 505 aa.	9.30E-280	12
845	cg43975720	3917	CATCCACCCAGCA CCAAGATGACC GGTA/CJCCITTTA CCAATTTGAGGC TGC GTG	A	C	Thr	Pro (1218)	NON- CONSERVATI VE	kinesin	Human Gene SWISSPROT- ID:Q12756 KINESIN-LIKE PROTEIN KIF1A (AXONAL TRANSPORTER OF SYNAPTIC VESICLES) - HOMO SAPIENS (HUMAN), 1690 aa.	0.00E+00	2
846	cg44013875	1710	GCCATGGAGAG GCTGCAGGAGA CAGTA/GJGAAGA TTATAGCTGAGC TGAACGAG	A	G	Glu	Gly (1219)	NON- CONSERVATI VE	kinesin	Human Gene SWISSNEW-ID:Q43896 KINESIN-LIKE PROTEIN KIF1C - HOMO SAPIENS (HUMAN), 1103 aa. pcds:TREMBLNEW-ID:G2738149 KINESIN-LIKE MOTOR PROTEIN KIF1C - HOMO SAPIENS (HUMAN), 1103 aa.	0.00E+00	
847	cg44009224	2806	TTTGGATCCTGA AAATGTTGTATTT T/CJATGTTGGAG GTTACCCACCTG ATTT	T	C	Tyr	His (1220)	NON- CONSERVATI VE	laminin	Human Gene SWISSPROT- ID:Q16787 LAMININ ALPHA-3 CHAIN PRECURSOR (EPILIGRIN 170 KD SUBUNIT) (E170) - HOMO SAPIENS (HUMAN), 1713 aa.	0.00E+00	
848	cg42930646	1228	TGATGCGGATAG CGTATGGATGGA ATA/GITGGACGA TGAGGAGGACC TGCCTTC	A	G	Met	Val (1221)	NON- CONSERVATI VE	laminin	Human Gene SWISSPROT- ID:P07221 CALSEQUESTRAIN, SKELETAL MUSCLE ISOFORM PRECURSOR (ASPARTACTIN) (LAMININ-BINDING PROTEIN) - ORYCTOLAGUS CUNICULUS (RABBIT), 395 aa.	1.80E-198	1

849	cg43935885	3745	CCAGACAGCAC CACTGGAACCC CTC/TCTTAGCAG CGCACAGACC CGAAGAAC	C	T	Pro	Leu (1222)	NON- CONSERVATI VE	MHC	Human Gene SPTREMBL-ID:P79457 MALE-SPECIFIC HISTOCOMPATIBILITY ANTIGEN H- YDB - MUS MUSCULUS (MOUSE), 1186 aa.	7.20E-173	
850	cg42928872	1807	GAGCTGCAGAG GAGGCTGGACC AGT/C/TTCATTGG GAAGCCCTCACT GTTTCATC	C	T	Ser	Phe (1223)	NON- CONSERVATI VE	misc_cha nnel	Human Gene TREMBLNEW- ID:G2465531 KIDNEY AND CARDIAC VOLTAGE DEPENDENT K+ CHANNEL - HOMO SAPIENS (HUMAN), 676 aa.	0.00E+00	11
851	cg44019843	929	GAGTGACCCGC CTCCCTGGTCCA AG/A/TJATGTGGA GTACACCTTCAC AGGGAT	A	T	Asn	Tyr. (1224)	NON- CONSERVATI VE	misc_cha nnel	Human Gene SPTREMBL-ID:Q15478 SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 1836 aa.	0.00E+00	17 (17q23.1)
852	cg44128805	1396	AGTGCACACAGT GAGCTCAGAGC TT/C/TJCCCTGA AAACCGAAAGTT TCAACT	C	T	Glu	Lys (1225)	NON- CONSERVATI VE	nuclease	Human Gene Similar to SWISSPROT- ID:P54278 PMS1 PROTEIN HOMOLOG 2 (DNA MISMATCH REPAIR PROTEIN PMS2) - HOMO SAPIENS (HUMAN), 862 aa.	1.60E-76	7
853	cg38642684	304	TTTCTGATAATC ATTTAAGGTATG T/TJAGTTGCTA GTATTTAATTTAA CCTT	A	T	Leu	End (1226)	NON- CONSERVATI VE	nuclease	Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pols:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	2.60E-50	

854 cg38642684	417	CTTTTCAGGTG CAATGATTAAAC C/A/TCTTAACTG TGCATTCCCTTAT GACAG	A	T	Ser	Arg (1227)	NON- CONSERVATIVE	nuclease	Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.pcds:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	2.60E-50	
855 cg44913844	1194	CCAGTTGGTAAA CTGGTCTTAAAC C/G/A/GAATCCA GTTAATTACTTT GCTGAG	G	A	Arg	Gln (1228)	NON- CONSERVATIVE	peroxidase	Human Gene SWISSPROT- ID:P04040 CATALASE (EC 1.11.1.6) - HOMO SAPIENS (HUMAN), 527 aa.	2.70E-296	11 (11p13)
856 cg40084915	5005	CCTGCGGTCTG GGGAGATGAGG GCC/T/CjCAAAC AGCACCTGATAT TCATTGGG	T	C	Glu	Gly (1229)	NON- CONSERVATIVE	phosphatase	Human Gene SPTREMBL-ID:O00197 RECEPTOR PROTEIN TYROSINE PHOSPHATASE HPTP-J PRECURSOR - HOMO SAPIENS (HUMAN), 1436 aa.	0.00E+00	1
857 cg42720088	214	AAAGCTCAGAGA GATCTGGGCTAT G/A/TjGCCACTT GTCAGCTGGGA GGAAGCC	A	T	Glu	Val (1230)	NON- CONSERVATIVE	reductase	Human Gene Similar to SWISSPROT- ID:P22072 3 BETA- HYDROXYSTEROID DEHYDROGENASE/DELTA 5->4- ISOMERASE TYPE II (3BETA-HSD II) (3-BETA-HYDROXY-DELTA(5)- STEROID DEHYDROGENASE (EC 1.1.1.145) (3-BETA-HYDROXY-5-ENE STEROID DEHYDROGENASE) (PROGESTERONE REDUCTASE) / STEROID DELTA-ISOMERASE (EC 5.3.3.1) (DELTA-5-3-KETOSTEROID ISOMERASE)) - RATTUS NORVEGICUS (RAT), 372 aa.	2.40E-50	

858	cg43957486	1528	CGCTCCTGCAC CGCATCCGCGA CGC[AT]GTCCT GCAACGACCTCT GCGAGCAC	A	T	Gln	Leu (1231)	NON- CONSERVATI VE	struct	Human Gene SWISSPROT- ID:P07204 THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN) - HOMO SAPIENS (HUMAN), 575 aa.	0.00E+00	20 (20p11.2)
859	cg40148056	1462	CTCAGAGACCC CTAACAAACCCAG CA[G/C]CCACAG AGCGGAACACTT AAGGATC	G	C	Gln	His (1232)	NON- CONSERVATI VE	struct	Human Gene SPTREMBL-ID:Q92777 SYNAPSIN IIB - HOMO SAPIENS (HUMAN), 478 aa.	2.90E-260	3 (3p)
860	cg43981852	473	CACCTCCTCCAG CTTCCCAGCCTC C[C/T]CGGCTCT GGCCAGGGCTGC CGCTGGG	C	T	Gly	Glu (1233)	NON- CONSERVATI VE	struct	Human Gene Homologous to SWISSPROT-ID:Q92176 CORONIN- LIKE PROTEIN P57 - BOS TAURUS (BOVINE), 461 aa.	7.80E-113	
861	cg42522566	318	GCAGCCAAAGAT CATCAAAGTGAA GA[A/G]CGTAA GGACCCGGGAGG ATGTGAAG	A	G	Asn	Ser (1234)	NON- CONSERVATI VE	struct	Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa.	6.00E-55	
862	cg43297806	966	ATAGTAGCCAGG GACAAGACAGC GG[T/C]TCTGCA GGGAGCGTAGT GCCAGAGG	T	C	Asn	Ser (1235)	NON- CONSERVATI VE	sulfotran sferase	Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa.jpcls:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa.	0.00E+00	10

863	cg43297806	994	TGCAGGGAGCG TAGTGCCAGAG GGGTCCTGGG AGGAGGCTGAA ATCACCTGA	T	C	Thr	Ala (1236)	NON- CONSERVATI VE	sulfotran sferase	Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa.	0.00E+00	10
864	cg43987111	1337	AGTAGTCTGCGT CTCCATAGAGTT TTC/AJCTCATGAC TGAGTTCTTGGT CTGGA	C	A	Arg	Ser (1237)	NON- CONSERVATI VE	synthase	Human Gene SWISSPROT- ID:P17812 CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE) - HOMO SAPIENS (HUMAN), 591 aa.	0.00E+00	18 (1p34.1)
865	cg43976335	633	GAAATGCACCTGG G ACCACTCGGGC AG[G/A]GCTGCC AGCCCGTAGCA GGCAATTC	G	A	Pro	Ser (1238)	NON- CONSERVATI VE	synthase	Human Gene SWISSPROT- ID:P48637 GLUTATHIONE SYNTHETASE (EC 6.3.2.3) (GLUTATHIONE SYNTHASE) (GSH SYNTHETASE) (GSH-S) - HOMO SAPIENS (HUMAN), 474 aa.	5.30E-240 (20q11.2)	20
866	cg39515668	605	ACGCACGAACC GGTCATACTGGT CG[G/T]TGATCC AGGAACGGTCG CACAGCTG	G	T	Thr	Asn (1239)	NON- CONSERVATI VE	synthase	Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCIN AMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa.	2.80E-72	
867	cg44027791	1261	GAAGCGCTTCTGT T ACACTGGGCGC ACT/CJCGAAGC GTTTGTCCTCCCTG TGTGGGT	T	C	Glu	Gly (1240)	NON- CONSERVATI VE	transcript factor	Human Gene SWISSPROT- ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	17

868	cg43992817	578	GAGGGGCCGCT GGAAGGTGACA CTGCTGTGTGG GGCCACGGAG GTGCCGCTG	C	T	Ala	Thr (1241)	NON- CONSERVATIVE	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q14469 TRANSCRIPTION FACTOR HES-1 (HAIRY AND ENHANCER OF SPLIT 1) (HAIRY-LIKE) (HHL) (HAIRY HOMOLOG) - HOMO SAPIENS (HUMAN), 280 aa.	1.50E-144	3
869	cg43297259	816	TAAGTGCTGAT GAGGTGTGACTT CTTCGGCTAAA GCCTTGCTCACA CTCCCT	T	C	Gln	Arg (1242)	NON- CONSERVATIVE	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. pcls:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	7.80E-54	
870	cg42716761	1594	CGAGAAGACCC TATACCATCACG TGTCGACGGCT GCGACGTGTTT CACCTCCG	C	G	His	Asp (1243)	NON- CONSERVATIVE	transcript factor	Human Gene SWISSNEW-ID:Q61079 SINGLE-MINDED HOMOLOG 2 (SIM) TRANSCRIPTION FACTOR (MSIM) - MUS MUSCULUS (MOUSE), 657 aa. pcls:SWISSPROT-ID:Q61079 SINGLE-MINDED HOMOLOG 2 (SIM) TRANSCRIPTION FACTOR (MSIM) - MUS MUSCULUS (MOUSE), 657 aa.	5.7e-312	21
871	cg42166807	2828	AGAGCAATGGCT CTCTCACTCCG TGTGAGAGTTGT CCTCTCAGAAGC TGGGC	G	A	Trp	End (1244)	NON- CONSERVATIVE	transferase	Human Gene SWISSPROT- ID:Q09328 ALPHA-1,3(6)- MANNOSYLGLYCOPROTEIN BETA- 1,6-N-ACETYL- GLUCOSAMINYLTRANSFERASE V (EC 2.4.1.155) (ALPHA-MANNOSIDE BETA-1,6-N- ACETYLGLUCOSAMINYLTRANSFER- ASE) (N-ACETYLGLUCOSAMINYL- TRANSFERASE V) (GNT-V) (GLCNAC-T V) - HOMO SAPIENS (HUMAN), 741 aa.	0.00E+00	2 (2q21)

872	cg38869466	752	TTCACCTTGTTATTA ACGTCCTGGTCC T/CIGGGCTTCAT AATGGTGTCAGG ATTT	C	Leu	Pro (1245)	NON- CONSERVATI VE	transport	Human Gene SWISSPROT- ID:P30825 HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG) - HOMO SAPIENS (HUMAN), 629 aa.	0.00E+00	13
873	cg42742340	3392	CAGAGAGACGG TGTCATCAGCA TC/C/TJGGGCCT CCCTGCAGCAG ACCCAGGC	T	Arg	Trp (1246)	NON- CONSERVATI VE	transport	Human Gene SWISSPROT- ID:Q04671 P PROTEIN (MELANOCYTE-SPECIFIC TRANSPORTER PROTEIN) - HOMO SAPIENS (HUMAN), 838 aa.	0.00E+00	15
874	cg43976701	513	TGGTATATCTGA ACTGAATCAGCC T/G/CJCTGAACCT TTACCTCAGTTT TCTAG	C	Ala	Pro (1247)	NON- CONSERVATI VE	transport	Human Gene SWISSPROT- ID:Q15436 PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM A - HOMO SAPIENS (HUMAN), 765 aa.	0.00E+00	
875	cg43920728	2024	GTAAGTCTCATT GTAAAATTGTTG C/A/GJTGAGCAG TGCTGGGGAGTT GACAGC	G	Cys	Arg (1248)	NON- CONSERVATI VE	transport	Human Gene SWISSPROT- ID:P22732 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER) - HOMO SAPIENS (HUMAN), 501 aa.	2.90E-237	1 (1p31)
876	cg43920728	2185	TGCTTGCTCTGG AAGGGCAGAGT GC/C/TJGCTCAC CTCCTTTTAGCC AAAGTAA	T	Arg	Gln (1249)	NON- CONSERVATI VE	transport	Human Gene SWISSPROT- ID:P22732 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER) - HOMO SAPIENS (HUMAN), 501 aa.	2.90E-237	1 (1p31)

877	cg42339179	450	TCCTCCACCAGG GTCATTTTGGCG TIG/AJTAAAG TTCCAGTGATCT CAATG	G	A	His	Tyr (1250)	NON- CONSERVATI VE	transport	Human Gene Homologous to SWISSNEW-ID:Q60714 LONG- CHAIN FATTY ACID TRANSPORT PROTEIN (FATP) - MUS MUSCULUS (MOUSE), 646 aa.[pcls:SWISSPROT- ID:Q60714 LONG-CHAIN FATTY ACID TRANSPORT PROTEIN (FATP) MUS MUSCULUS (MOUSE), 646 aa.	1.90E+05	15
878	cg17663981	383	TGCACCTGCCA CCAAAACCCCTG CA[G/A]CTGCC CAAAGGGGATG TCAACTAC	G	A	Ser	Asn (1251)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.2 3)
879	cg43918356	1806	GCTCCCGTGCA CGGGGCTGTAG CGC[C/T]CAGGA CTGCCCAGGCC TGGCTTTGC	C	T	Gly	Glu (1252)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75176 KIAA0692 PROTEIN - HOMO SAPIENS (HUMAN), 783 aa (fragment).	0.00E+00	12
880	cg43924089	1080	ACCTCCTGGAG CAGTCCTGGTGT TA[C/T]ATCCCT GCCCTGGAGT TCCCACT	C	T	His	Tyr (1253)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA31589 KIAA0614 PROTEIN - HOMO SAPIENS (HUMAN), 1630 aa (fragment).	0.00E+00	12
881	cg43930961	2459	TTCTCCGTAGT CACAGACGTTAG G[C/T]TACTGCTT TCGGCTTCAATG GAAAC	C	T	Ser	Asn (1254)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA20772 KIAA0313 PROTEIN - HOMO SAPIENS (HUMAN), 1499 aa.	0.00E+00	4
882	cg43966528	680	AACAACACATTC AGTACAGTGCAG CIA/GJTATCAGCA GGCCAAAGTTAAC CAATC	A	G	Met	Thr (1255)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O00237 HKF-1 - HOMO SAPIENS (HUMAN), 685 aa.	0.00E+00	

883	cg43980727	1367	TCCTTCCTTGTA GTCAGAGACATC AIG/AJGAGAGTA ACTGGATGTTAG CTCCAA	G	A	Pro	Leu (1256)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P38432 P80-COILIN - Homo sapiens (Human), 576 aa.	0.00E+00	17
884	cg43981483	1540	TGACTGCATTAT TCGCAGCTGCTT AIA/GIGGACAAA TTCTACCTTCTT CTGGGT	A	G	Leu	Pro (1257)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q75882 ATTRACTIN - HOMO SAPIENS (HUMAN), 1198 aa.	0.00E+00	20
885	cg44932392	1200	TAGATGAAGGAG CCTGAGTAAGAG GIC/TJCACGCAC CAGCCTGTAGAA CATATA	C	T	Trp	End (1258)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD23581 CULLIN 2 - HOMO SAPIENS (HUMAN), 745 aa.	0.00E+00	
886	cg44932924	2754	AACAGTGAGTCG TCTCCAGCAGCA GAT/CJGGAGTT CTTGAACAGGCA GCTGTTG	T	C	Met	Thr (1259)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q92574 HAMARTIN (MYELOBLAST KIAA0243) - HOMO SAPIENS (HUMAN), 1164 aa.	0.00E+00	9
887	cg43985955	2082	ACCTCAAACCCC CTTTGGCCCTGT AT/CJCAGGAGC ACAGATACAGTT TATGTA	T	C	Ser	Pro (1260)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	2.70E-299	
888	cg44002507	1373	GTCGCACCTGG CAGCCAGCAGG ATC/C/TJCGGCTA TGTCACGCAG CCGGAGAA	C	T	Gly	Glu (1261)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD21812 G9A - HOMO SAPIENS (HUMAN), 1001 aa.	8.10E-298	
889	cg44002507	2870	TTTCCCTTCCTCT TGAGAAATTCTT T/CJCTTAATGCT GGATTCCGAAC CAGG	T	C	Lys	Glu (1262)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD21812 G9A - HOMO SAPIENS (HUMAN), 1001 aa.	8.10E-298	

890	cg44002507	507	CGCAGGTCCTG GTGGGCCATGA ACA/C/TGGGCA CGGGCACCAGG TTGGGCTCG	C	T	Val	Met (1263)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD21812 G9A - HOMO SAPIENS (HUMAN), 1001 aa.	8.10E-298	
891	cg44128920	1086	GAGCAGCAGCG AAAACGGCTTCA ACIA/CJGCAGTT GGAAGAACGCA GTCGTGAA	A	C	Gln	Pro (1264)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa.	1.00E-290	19
892	cg43968641	3315	TCATTCTCTCA GGGAACATATCA GIC/TJCAGAGAA ATATACAAGAAC ATTCT	C	T	Ala	Thr (1265)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q15043 MRNA (KIAA0062) FOR ORF (NOVEL PROTEIN), PARTIAL CDS - HOMO SAPIENS (HUMAN), 531 aa (fragment).	2.00E-285	8
893	cg43934178	2180	ACAAAGTAGTGG AACTTCTCTTG A/A/GJACAGTCC AGGGTGTGGCC CAGGACC	A	G	Phe	Leu (1266)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD29670 DNA TOPOISOMERASE III BETA - HOMO SAPIENS (HUMAN), 862 aa.	1.80E-274	
894	cg43934178	2596	CCAGGGCATGA CCTCCGTGAAG CCT[G/AJGTGAG AGGACGGTCTTC CCGGAGCA	G	A	Pro	Leu (1267)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD29670 DNA TOPOISOMERASE III BETA - HOMO SAPIENS (HUMAN), 862 aa.	1.80E-274	
895	cg43949042	378	GGACGTACATGA GGACGGCTATT GG[C/AJTGTCGG ATGATGAGCGAC AGCCACA	C	A	Gln	His (1268)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75907 ACAT RELATED GENE PRODUCT 1 - HOMO SAPIENS (HUMAN), 488 aa.	6.10E-268	
896	cg43916582	2097	CCTTCATCTTTAT TCTGCTGCTCAG T/TGJTCCATTGG TTCCTCTTGATT CGGT	T	G	Thr	Pro (1269)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75475 LENS EPITHELIUM- DERIVED GROWTH FACTOR - HOMO SAPIENS (HUMAN), 530 aa.	2.30E-259	

897	cg43258841	485	A	G	Ile	Thr (1270)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa...	2.70E-258	
898	cg43979679	619	C	T	Gln	End (1271)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13977 MAJOR YO PARANEOPLASTIC ANTIGEN - HOMO SAPIENS (HUMAN), 509 aa (fragment).	5.60E-258	16 (16p13.1)
899	cg42202923	887	A	G	Leu	Pro (1272)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75926 PROTEIN INHIBITOR OF ACTIVATED STAT PROTEIN PIASY - HOMO SAPIENS (HUMAN), 510 aa.	2.40E-256	
900	cg43320405	994	C	A	Met	Ile (1273)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB46424 DKFZP434G153 PROTEIN - HOMO SAPIENS (HUMAN), 466 aa.	8.20E-245	
901	cg43917689	3689	G	A	His	Tyr (1274)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q92551 MYELOBLAST KIAA0263 - HOMO SAPIENS (HUMAN), 441 aa.	3.50E-240	3
902	cg43922856	1546	G	A	Pro	Ser (1275)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa.	2.00E-237	12 (12q22)
903	cg43922856	1608	A	T	Met	Lys (1276)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa.	2.00E-237	12 (12q22)

904	cg43955639	505	CGTGTGGCAGG CATGGTGATGAG GG[G/A]TGCTGG GGCCAGGGGAGG TGGCAGGA	G	A	Pro	Ser (1277)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O15417 CAGL79 - HOMO SAPIENS (HUMAN), 413 aa (fragment).	2.80E-215	
905	cg43950766	991	AGGAATGACCAAT AGCACCTGGGT CA[T/C]ACTTGTC CACCCACTCTTT AATTTT	T	C	Tyr	Cys (1278)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD44491 PTD004 - HOMO SAPIENS (HUMAN), 396 aa.	5.30E-214	22
906	cg43985159	2102	ACTTCTGCCTTC AGCTGCAAAACC A[G/A]AGGACGG CATCCGAGGACT GAACGC	G	A	Ser	Phe (1279)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q15018 ORF - HOMO SAPIENS (HUMAN), 419 aa (fragment).	1.30E-212	10
907	cg41022625	1136	CGTCTTCTCCAT CATTACATCAT C[G/T]CCACCCT GCTCCTCAGCAC GCAGCT	G	T	Ala	Ser (1280)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34036 CGI-40 PROTEIN - HOMO SAPIENS (HUMAN), 845 aa.	2.00E-207	11
908	cg44002669	1438	ACCTTGGCGCTTG CACTCGCGGCA GC[C/T]CCTGTC CAGTTCCTCCTT CTCCTTC	C	T	Gly	Ser (1281)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q16543 CDC37 HOMOLOG - HOMO SAPIENS (HUMAN), 378 aa.	8.80E-205	
909	cg44128902	675	CCGGGATCGAG ACAGAGACAGA GAG[C/G]GGGAC AGGGATCGGGA TCGGGATCG	C	G	Arg	Gly (1282)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1.00E-201	1 (1p36.2)
910	cg44129213	1413	GGGTGTGGACT GGCTGCAGATG TCAT[C/T]TGTA TTCAGATTCTTT CTGGCGA	T	C	Met	Val (1283)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O88466 ZINC FINGER PROTEIN 106 - MUS MUSCULUS (MOUSE), 1888 aa.	5.60E-194	

911	cg43996402	684	CTTCTCCGGCTC CTTCTCCTCCCTG C/C/A/GTGGCTT CTGCTGCTCCCC TCCTTT	C	A	Gly	Cys (1284)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q12804 RECEPTIN - HOMO SAPIENS (HUMAN), 451 aa.	2.60E-189	2
912	cg43984909	1268	CGAATATCAGCT GCATCCAGTGTC C/C/TTCAGACGA GAATACAAGCCA AGGCCT	C	T	Pro	Leu (1285)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q99963 PROTEIN CONTAINING SH3 DOMAIN, SH3GL3 - HOMO SAPIENS (HUMAN), 347 aa.	1.70E-187	15
913	cg42910688	778	GACAGAGGACA TTCCCATAAATTT G/G/TJTGCAA CAAAAGTGACTT AGTGCG	G	T	Val	Phe (1286)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P55040 GTP-BINDING PROTEIN GEM (GTP-BINDING MITOGEN-INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR) Homo sapiens (Human), 296 aa.	7.70E-158	8
914	cg43950590	1351	AAGAATCCTCCG ACGGCTTCGTTA C/C/TJATCCTGTC TGAAGCGGATTG CACGA	C	T	Gly	Ser (1287)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa.	1.90E-154	7
915	cg44931503	945	TTTTAAAGAGTT CATATAATCAT G/A/GJGGTCTTC AAATACCGTTGT TCCTTC	A	G	Leu	Pro (1288)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34078 CGI-83 PROTEIN - HOMO SAPIENS (HUMAN), 288 aa.	5.00E-154	
916	cg43303845	774	ACATTGCCTAGA CAAAACTCACAA C/T/CJACCTGCTC AAGTCAAAATG GCCCA	T	C	Leu	Pro (1289)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O93263 AVENA - GALLUS GALLUS (CHICKEN), 550 aa.	1.90E-138	
917	cg43973762	117	AGCTGAACAACA GAAGTTGTGGAA T/G/TJAGGAGTTA AAATATGCCAGA GGCAA	G	T	Glu	End (1290)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14777 RETINOBLASTOMA-ASSOCIATED PROTEIN HEC - HOMO SAPIENS (HUMAN), 642 aa.	2.20E-137	

918	cg43973762	165	CAAAGAAGCGAT TGAAACACAAATT A[G/C]CAGAGTA TCACAAATTGGC TAGAAA	G	C	Ala	Pro (1291)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14777 RETINOBLASTOMA-ASSOCIATED PROTEIN HEC - HOMO SAPIENS (HUMAN), 642 aa.	2.20E-137	
919	cg43973762	376	GCCCTAAATAAA AAAATGGGTTTG G[A/G]GGATACT TTAGAACAATTG AATGCA	A	G	Glu	Gly (1292)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14777 RETINOBLASTOMA-ASSOCIATED PROTEIN HEC - HOMO SAPIENS (HUMAN), 642 aa.	2.20E-137	
920	cg42910848	443	CCATGGTGCCA GGCCGTGCTCC CCA[G/C]GTGCC TCCGGGGTGCT GAAGATCTT	G	C	Pro	Arg (1293)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14988 GTPASE- ACTIVATING PROTEIN - HOMO SAPIENS (HUMAN), 308 aa (fragment).	3.10E-132	
921	cg29351416	537	TTTCCCAAAAGT TCCAAGTAGACA A[C/G]AGTAATC GCCTGTTACTGC AGCAGG	C	G	Asn	Lys (1294)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa.	3.20E-127	
922	cg29351416	574	GTTACTGCAGCA GGTCTCATTACC A[G/T]ACATTCCT GGGAACATATACC GTCAG	G	T	Asp	Tyr (1295)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa.	3.20E-127	

923	cg43938372	481	TTGTTTCCCACT TAATTTATTTTTT CTCTGCTTGTT CTTCTTCTTCAT CCT	C	T	Gly	Glu (1296)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD40376 PTD013 - HOMO SAPIENS (HUMAN), 243 aa.	1.50E-123	
924	cg44930828	658	CCTCAAGGTTTC GCTGCCGAAGC TTTG/AJCCAACGT GCAGCTCCTGG ATACCGA	G	A	Ala	Thr (1297)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET- ACTIVATING FACTOR ACETYLDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa.	3.10E-122	
925	cg44930828	680	CTTGCCAACGTG CAGCTCCTGGAT A/C/TJCGACGGG GGTTTGTGCAC TCGGAC	C	T	Thr	Ile (1298)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET- ACTIVATING FACTOR ACETYLDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa.	3.10E-122	
926	cg44035718	919	CTGGAGTACCA GGAAGAACTGA GGTIC/TJCCACTA CAAGGACATGCT CAGCGAA	C	T	Ser	Phe (1299)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA83010 KIAA1058 PROTEIN - HOMO SAPIENS (HUMAN), 1534 aa (fragment).	2.20E-121	2
927	cg44921277	571	TTGGCGCAACTT CCCCATCACCTT C/G/AJCCCTGCTAT GCGGCCCTCTT CTGCCT	G	A	Ala	Thr (1300)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q35682 MYELOID UPREGULATED PROTEIN - Mus musculus (Mouse), 296 aa.	1.70E-120	

928	cg43250166	461	GCCGTGATTGTC TCCAGTGCCATC TTC/TGTGCAGAT GCTCATCTCGGC TCTCG	C	T	Glu	Lys (1301)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43382 HYPOTHETICAL 146.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 1296 aa.	3.30E-102	2
929	cg39512856	344	CTTTTCCAGGC TTCAGCAACGA GIG/AJTTCCTCC TTCGTTGCAATT TCCAG	G	A	Thr	Ile (1302)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	
930	cg39512856	517	GCCGTCCACTT CTGATATCCCC TTC/TCCGGCGA TAACCAGGTAAA ATTTTC	C	T	Gly	Glu (1303)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	
931	cg39512856	536	TCCCCTCCCG CGATAACCAGGT AA/A/CJATTTCC GGTAACGGACC GAGTTCA	A	C	Phe	Val (1304)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	
932	cg39512856	638	TGGTCTTCAACG AGATGCCACGAT G[C/A]CTCATCAC TGTTGAAAACAG CCACA	C	A	Ala	Ser (1305)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	
933	cg39570960	851	GCCTCCAGGAA GTCGTTTGTGT TG[A/G]GCTGAA CGAATGTGCGTC CAGCCGC	A	G	Glu	Gly (1306)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14997 3-7 GENE PRODUCT - HOMO SAPIENS (HUMAN), 709 aa (fragment).	2.60E-93	
934	cg43980391	510	AGTAAATGGACA AGAATATCATCT TTC/TJAACTTGTA GACACAGCCGG GCAAGA	C	T	Gln	End (1307)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q15382 RAS-RELATED GTP- BINDING PROTEIN - HOMO SAPIENS (HUMAN), 184 aa.	2.10E-90	1

935	cg43983527	991	TTCTGGAAGGAT GGTGCAACCTG GT[G/T]CGGCCG CCATTACTGCGA GAGTCTG	G	T	Cys	Phe (1308)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47226 TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)] - Mus musculus (Mouse), 423 aa.	6.50E-90	3 (11q23.3)
936	cg42341305	114	GATGAATATTCG AGTACAGACACA C[C/T]GTATCCC GGCAGCCTACC TCCAGAA	C	T	Pro	Leu (1309)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60309 KIAA0563 PROTEIN - HOMO SAPIENS (HUMAN), 870 aa.	8.10E-90	
937	cg43980889	737	CTTCTATTTTGAAT TTCTAAAGACCA[T/G]TTACAAGTA GAAAATGATGCT TACC	T	G	His	Gln (1310)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	4.50E-89	
938	cg43980889	741	TATTTGAAATTC AAAGACCATTTA[C/T]AAGTAGAAA ATGATGCTTACC CTGG	C	T	Gln	End (1311)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	4.50E-89	
939	cg43980889	781	GCTTACCCTGGT A ACCGATAGAACA G[A/C]AAATGTTA AATATAGACAAG TGGAC	A	C	Glu	Ala (1312)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	4.50E-89	
940	cg29349483	146	GCAGTTTTTCAC CAAGATCAAGAC C[G/T]CTGACCA CCAGTACATGGA GGGCTT	G	T	Ala	Ser (1313)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q61081 CDC37 HOMOLOG - MUS MUSCULUS (MOUSE), 379 aa.	2.00E-88	
941	cg43918287	641	TCTATGGCATCA TCCTGCATGACC A[C/T]TTGTGCAT CTAAACCAGCCC AGCCG	C	T	Val	Met (1314)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P87891 GAG PROTEIN - HUMAN ENDOGENOUS RETROVIRUS K, 426 aa (fragment).	7.30E-84	

942	cg43918287	651	CATCCTGCATGA CCACTTGTGCAT CT/GJAAACCAG CCAGCCGCCA ACCCCA	T	G	Leu	Phe (1315)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P87891 GAG PROTEIN - HUMAN ENDOGENOUS RETROVIRUS K, 426 aa (fragment).	7.30E-84	
943	cg43918287	676	TAAACCAGCCCA GCCGCCAACCC CCJA/GJAAAGTT GGTCTGCAGTTA TATTAAT	A	G	Leu	Ser (1316)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P87891 GAG PROTEIN - HUMAN ENDOGENOUS RETROVIRUS K, 426 aa (fragment).	7.30E-84	
944	cg43918287	693	CAACCCCAAAA GTTGGTCTGCAG TT/CJATATTAAAT TGAGTTGGAC CTGGG	T	C	Ile	Met (1317)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P87891 GAG PROTEIN - HUMAN ENDOGENOUS RETROVIRUS K, 426 aa (fragment).	7.30E-84	
945	cg37027086	217	GAATCAGAACTA CAAGGATCAATT A/T/CJCCAGCT CAATGTCAGGGT TCITCA	T	C	Ser	Pro (1318)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA76824 KIAA0980 PROTEIN - HOMO SAPIENS (HUMAN), 1406 aa (fragment).	1.20E-83	
946	cg42688841	430	ATTATAACTGGG ATCCAGTCAAC A/T/AJAGGTAGA ATTTCATTAACT CAAG	T	A	Met	Leu (1319)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (Cl- SGDH) - Bos taurus (Bovine), 189 aa.	1.90E-83	
947	cg42688841	598	CCGAGCCTAGT GCCAGCGCGGC GGC/A/CJAGACA GAGCTGTCAGA GCGGCGACC	A	C	Cys	Gly (1320)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (Cl- SGDH) - Bos taurus (Bovine), 189 aa.	1.90E-83	
948	cg40332814	399	ACTGCACAGGG ACCGAATCTCTG CC/T/CJCCCGCT CTGCAGCCAGG TGCTCCAA	T	C	Glu	Gly (1321)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA74864 KIAA0841 PROTEIN - HOMO SAPIENS (HUMAN), 641 aa (fragment).	3.10E-83	19

949	cg43920571	2059	GCGTTTTTCTCT CACGTCCGCTCTG A/G/AJATTACTG AGGAATATTGTG CTGGC	G	A	Ser	Phe (1322)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P34624 HYPOTHETICAL 63.5 KD PROTEIN ZK353.1 IN CHROMOSOME III - Caenorhabditis elegans, 548 aa.	3.50E-82	10
950	cg44024149	451	GGAAGCCGCAC TCAGTTATGGCT TCIT/CJACGGCT GCCACTGTGGC GTGGGTGG	T	C	Tyr	His (1323)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P14555 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) (GROUP II PHOSPHOLIPASE A2) - Homo sapiens (Human), 144 aa.	5.30E-79	1 (1p35)
951	cg43307245	156	GATATGATAGCT TGTCCTGAACT G/A/GJACTCCT GCCGTGATAAC GTGTGAC	A	G	Glu	Gly (1324)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15488 GLYCOGENIN-2 ALPHA - HOMO SAPIENS (HUMAN), 501 aa.	1.00E-75	X
952	cg39523553	698	GTGTGAGGTCTG CCCGATCCGG ATG/AJGCTGCC GGTGGGTGATC GACGGTAG	G	A	Gly	Ser (1325)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.20E-75	
953	cg39523553	861	ATGGCTCTTTCC GCCTGGCCCGA GC/T/CJCGATCA GGCATCAAGGT GCCTGGAA	T	C	Leu	Pro (1326)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.20E-75	
954	cg35933325	312	ACCAATGCCAC TATTTTTCTCCC [A/C]TTGCGAAAA ATGAAGGAAATC ACGT	A	C	Asn	Lys (1327)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA74845 KIAA0822 PROTEIN - HOMO SAPIENS (HUMAN), 1581 aa.	2.40E-74	

955	cg41677120	325	CACGACCCACG AGATCATGGGG CCCA/GIAGAAA AAGCACCTGGA CTACTTAAT	A	G	Lys	Glu (1328)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	1.10E-71	11
956	cg41677120	330	CCACGAGATCA TGGGGCCCAAG AA/CJAAGCAC CTGGACTACTTA ATTCAGT	A	C	Lys	Asn (1329)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	1.10E-71	11
957	cg41677120	382	CACAAATGAGAT GAATGTGAACAT C/C/TJACAGTTG GCAGACAGTTTA TTTGA	C	T	Pro	Ser (1330)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	1.10E-71	11
958	cg39648832	208	TGCAGCCTCGTC CTCCTCCTCTGG C/ATJGGCTCTG CACACTCTGCTC CTGGTA	A	T	Leu	Gln (1331)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA76807 KIAA0963 PROTEIN - HOMO SAPIENS (HUMAN), 1366 aa.	3.20E-70	
959	cg42696021	412	GACACCCGGAC CCGGGCATGCT TCA/C/GJACAGT GGCTGTGCGCG CTTCACAAT	C	G	Thr	Arg (1332)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
960	cg42696021	421	ACCCGGGCATG CTTCACACAGTG GC/T/CJGTGCCG CCTTCACAATGA AGTGAAC	T	C	Leu	Pro (1333)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
961	cg34243633	269	CAGAGATAATGC AGGCCAGGGAG GA/G/CJATTGCA CTGGATGTCACC ATCATGG	G	C	Ile	Met (1334)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa.	1.30E-68	

962	cg34243633	453	ACGACATAAGAC ACTTGTTTCCCA G[C/T]TGGGGAG CAGCATGGCAA CCAGTGT	T	Ser	Asn (1335)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa.	1.30E-68	
963	cg43942922	308	CCTGAGCTCCA GCCTCCACCTC CAIC/GIAGACCA GCCTGTCACCTC TGAGCCC	G	Thr	Arg (1336)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.30E-68	
964	cg43942922	317	CAGCCTTCCACC TCCACAGACCAG C[C/T]TGTACCT CTGAGCCCACAT CTCAG	T	Pro	Leu (1337)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.30E-68	
965	cg43942922	325	CACCTCCACAGA CCAGCCTGTAC C[T/C]CTGAGCC CACATCTCAGGC CACTAG	C	Ser	Pro (1338)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.30E-68	
966	cg43942922	341	CCTGTCACCTCT GAGCCACATCT C[A/G]GGCCACT AGGGGAAGAAA AAATAGG	G	Gln	Arg (1339)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.30E-68	
967	cg35133436	291	TTCTCTAGTCCA CCAGGAGGCTA CAI/GJCTCGGC TCTCAGGGTCAG GTAATGA	G	Thr	Ala (1340)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60309 KIAA0563 PROTEIN - HOMO SAPIENS (HUMAN), 870 aa.	2.10E-66	

968	cg44938009	1289	GAGTGCACGCA TAAAGATGGAAG AG[G]TATGCACT ACTTTCIGATCC AGTGGA	G	T	Asp	Tyr (1341)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O43182 RHO-GTPASE- ACTIVATING PROTEIN 6 (RHO-TYPE GTPASE-ACTIVATING PROTEIN RHOGAPX-1) - Homo sapiens (Human), 587 aa.	5.80E-66	X
969	cg43949821	287	ATTTTAATTCCTT CCTGTCTACGGC [G/A]GTTGGACC TCCTGGCTCTCT GCTGT	G	A	Arg	Cys (1342)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34394 NUCLEAR PORE COMPLEX INTERACTING PROTEIN NPIP - HOMO SAPIENS (HUMAN), 350 aa.	3.80E-62	
970	cg39516123	681	TGGCTTCGGCTG GCGGGCCATCA AT[C/T]CCAGCAT GGCTGCCCCCA GCAGTCC	C	T	Pro	Ser (1343)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa.	5.10E-62	
971	cg42731307	347	CGAAAAGCAAAG TGCAGTTTGTG C[T/C]TCGGCTG TTGAGTGGTTCTG GGTCCA	T	C	Ser	Gly (1344)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa.	2.60E-61	
972	cg42731307	488	TCTGGAAAGAAG GCATTGATGATC C[G/A]GTCCCCC AGTGGGTTGATG GCAAGT	G	A	Arg	Trp (1345)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa.	2.60E-61	
973	cg42731307	524	GGGTTGATGGC AAGTTCTGGAAT CC[T/C]CTGGAA ATCTCCCGGCT GAGAGTC	T	C	Arg	Gly (1346)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa.	2.60E-61	

974	cg44910937	648	TGCCTTTGGAAC AGGAATATGAAA A/G/TJAAACTCAG AGCCGAGTTAGT GGAAA	G	T	Lys	Asn (1347)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20716 F53B7.3 - CAENORHABDITIS ELEGANS, 267 aa.	2.60E-61	3
975	cg43335624	149	TCGAAAGGAAGT GAGTGCAGATG GGI/A/GJAGACCA TCACTGTCACTT TCITTTAA	A	G	Lys	Glu (1348)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62184 T-COMPLEX PROTEIN 10C (TCP-10) - MUS MUSCULUS (MOUSE), 438 aa.	7.00E-61	
976	cg43277268	448	CGCTAATGCCAA GAAGGAGATGG TGIC/A/GCTCCA AGCTGCCCAACA GTGTGCT	C	A	Arg	Ser (1349)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD45423 EH DOMAIN- CONTAINING PROTEIN EHD1 - MUS MUSCULUS (MOUSE), 534 aa.	3.90E-60	
977	cg44128084	724	CTTGACATCCAG CCAGACGGTTCA G/A/GJATCAGCG GTTCTGTGGTGC GACGGG	A	G	Glu	Gly (1350)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa.	1.70E-59	
978	cg30455661	322	TTCTCAAGTGGT TTGAAGTCAAAC A/G/TJATTTCAAC AGAAGAAATCAG CCCTC	G	T	Gln	His (1351)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14185 DOCK180 PROTEIN - HOMO SAPIENS (HUMAN), 1865 aa.	5.20E-58	
979	cg42747615	31	TGTGATAAAAAGT CACTTTTCAGGCC A/T/CJTCACAGC GAATCTTCAGAC ACTTTT	T	C	Ile	Thr (1352)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14693 HYPOTHETICAL PROTEIN KIAA0188 - Homo sapiens (Human), 899 aa (fragment).	1.60E-57	
980	cg43153425	276	ACAAATTAATCTAT GGGTTCTACTGA A/T/GJCTCGGT TGACTACATGGG CTCAAG	T	G	Ser	Ala (1353)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment).	2.40E-57	

981	cg43968980	1093	TATTTTCTGCTTC TCTAACAGCTGA [C/A]TGTGAATTG CTTCCTTGGACT GAAG	A	Ser	Ile (1354)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.50E-56	5
982	cg30384142	173	GATAGTGGTGTA TGGTGATGCGA GT[A/T]AACCTGA CGAATGGTTAGC TGAAAT	T	Lys	End (1355)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P44788 SUN PROTEIN (FMU PROTEIN) - Haemophilus influenzae, 451 aa.	5.30E-56	
983	cg43957773	445	GGGCTCACCGT AGAGCAACTGCA AT[C/A]GCTCTG GGCCTGGGCCT GGACAGGA	A	Asp	Tyr (1356)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43914 DNAX ACTIVATION PROTEIN 12 - HOMO SAPIENS (HUMAN), 113 aa.	3.30E-54	19
984	cg43931038	464	AGGGCAACTTGT GGGCAACCTGG TC[A/C]AGGAAA CCTTGACTTCTT CAAATTC	C	Leu	Trp (1357)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa.	6.10E-54	11
985	cg43931038	588	CCTCCCCCATGT CGATGCCCAACA C[T/C]TTTGGAG TGATGGGCTTGA AAGGG	C	Ser	Gly (1358)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa.	6.10E-54	11
986	cg43971060	686	CCCACCTCGTTC GTGCTCCCAACC CT[C/T]CCCAGCT CCACCGCCTGG TCTTCAG	T	Pro	Ser (1359)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P31639 SODIUM/GLUCOSE COTRANSPORTER 2 (NA(+)/GLUCOSE COTRANSPORTER 2) (LOW AFFINITY SODIUM-GLUCOSE COTRANSPORTER) - Homo sapiens (Human), 672 aa.	4.20E-53	

987	cg44010070	541	TTCTCTGCCGGC ACCTACCCGCG CC[T/G]GGAGGA GTACCGCCGGG GCATCTTA	G	Leu	Arg (1360)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O35775 SYNCOLLIN (SIP9) - Rattus norvegicus (Rat), 145 aa.	6.40E-51	
988	cg43298242	145	TCTGTTGGCAGG GCTCACAGAGA CG[G/A]GGGTGA GGGGAGAGATC GTGGGTTC	A	Pro	Leu (1361)	NON- CONSERVATI VE	water_ch annel	Human Gene SWISSPROT- ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa.	1.30E-163	
989	cg43298242	163	AGAGACGGGG TGAGGGGAGAG ATC[G/A]TGGGTT CATGAGATCCCA TC TTGGG	A	Thr	Met (1362)	NON- CONSERVATI VE	water_ch annel	Human Gene SWISSPROT- ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa.	1.30E-163	
990	cg43300636	440	CCACAGCCGCC ACGCCACCTC CCG[G/gap]CCCA GGCCAGGCCT ATGCGCATCA	gap	Gly	Gly (1363)	FRAMESHIFT	ATPase_ associate d	Human Gene SPTREMBL-ID:Q29466 VACUOLAR H+-ATPASE SUBUNIT (EC 3.6.1.34) (H(+)-TRANSPORTING ATP SYNTHASE) (H(+)- TRANSPORTING ATPASE) (MITOCHONDRIAL ATPASE) (CHLOROPLAST ATPASE) (COUPLING FACTORS (F(O), F(1) AND CF(1))) - BOS TAURUS (BOVINE), 838 aa.	1.70E-175	
991	cg43300636	446	CCGCCACGCC ACCTCCCGGCC CAG[G/gap]CCCA GGCCTATGCGC ATCACCATGG	gap	Gly	Gly (1364)	FRAMESHIFT	ATPase_ associate d	Human Gene SPTREMBL-ID:Q29466 VACUOLAR H+-ATPASE SUBUNIT (EC 3.6.1.34) (H(+)-TRANSPORTING ATP SYNTHASE) (H(+)- TRANSPORTING ATPASE) (MITOCHONDRIAL ATPASE) (CHLOROPLAST ATPASE) (COUPLING FACTORS (F(O), F(1) AND CF(1))) - BOS TAURUS (BOVINE), 838 aa.	1.70E-175	

992	cg43250373	193	CTGTGGGGTTGAA CCCAGAACAAAG C[A/gap]TTGCCA GAAAACGTTAAG TATGGGA	gap	Leu	Cys (1365)	FRAMESHIFT	ATPase_ associate d	Human Gene Similar to TREMBLNEW- ID:G2921585 ECTO-ATPASE - MUS MUSCULUS (MOUSE), 495 aa.	1.40E-100	10 (10q24)
993	cg43132502	360	GGCCCCAGTGC AGTGGGTGGCA CCG[C/gap]CGAG GCTGCTGTTACG GCTCATCTT	gap	Pro	Arg (1366)	FRAMESHIFT	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE HOMO SAPIENS (HUMAN), 126 aa.	9.40E-58	11
994	cg42528468	284	GCTCCTGCCTG GGAACAACCGG AAG[G/gap]TGTA TGAAC TGAGCAA TGTGCAAGA	gap	Val	Cys (1367)	FRAMESHIFT	cadherin	Human Gene Similar to SWISSPROT- ID:P05362 INTERCELLULAR ADHESION MOLECULE-1 PRECURSOR (ICAM-1) (MAJOR GROUP RHINOVIRUS RECEPTOR) (CD54) - HOMO SAPIENS (HUMAN), 532 aa.	8.40E-78 (19p13.3)	19
995	cg43264626	1150	TTTGCCAGTTTT CTTCTTGAGTTG G[C/gap]CCTCCA GGCAACCCACA GAGCTAAA	gap	Gly	Ala (1368)	FRAMESHIFT	cathepsi n	Human Gene SWISSPROT- ID:P43235 CATHEPSIN K PRECURSOR (EC 3.4.22.38) (CATHEPSIN O) (CATHEPSIN X) (CATHEPSIN O2) - HOMO SAPIENS (HUMAN), 329 aa.	4.10E-183	1
996	cg43132668	1893	CGATGCGTGCC AGGGTGATTCC GGA[G/gap]GCC CGCTGGTGTTGT GAGGACCAAGC	gap	Gly	Ala (1369)	FRAMESHIFT	cathepsi n	Human Gene Similar to SWISSPROT- ID:P98119 SALIVARY PLASMINOGEN ACTIVATOR ALPHA 1 PRECURSOR (EC 3.4.21.68) (DSPA ALPHA-1) - DESMODUS ROTUNDUS (VAMPIRE BAT), 477 aa.	3.90E-74 5 (5q33)	5 (5q33)
997	cg43132668	1894	GATGCGTGCCA GGGTGATTCCG GAG[G/gap]CCC GCTGGTGTGTGA GGACCAAGCT	gap	Gly	Ala (1370)	FRAMESHIFT	cathepsi n	Human Gene Similar to SWISSPROT- ID:P98119 SALIVARY PLASMINOGEN ACTIVATOR ALPHA 1 PRECURSOR (EC 3.4.21.68) (DSPA ALPHA-1) - DESMODUS ROTUNDUS (VAMPIRE BAT), 477 aa.	3.90E-74 5 (5q33)	5 (5q33)

998	cg44924334	198	AAAGCTAATTGA GACCTATTCTC C[<i>gap</i>]AAACT ACCAAGACTATG AGTATCT	A	<i>gap</i>	Lys	Lys (1371)	FRAMESHIFT	glycoprotein	Human Gene Similar to SWISSPROT- ID:Q13491 NEURONAL MEMBRANE GLYCOPROTEIN M6-B - HOMO SAPIENS (HUMAN), 283 aa (fragment).	5.60E-76	
999	cg43303165	2549	GGCCCCCACTAT CAGGGGCCCTG GC[C <i>gap</i>]TCAAT CACTGAGACCAT CCAAGTCC	C	<i>gap</i>	Ser	Gln (1372)	FRAMESHIFT	histone	Human Gene Similar to SWISSPROT- ID:P53973 HISTONE DEACETYLASE HDA1 - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 706 aa.	4.10E-70	X
1000	cg42489148	881	TGCGAGTGGAT GCGGAACCGGC GCA[G <i>gap</i>]CAGT CCCTCGGCAGC CAAGTGAAAA	G	<i>gap</i>	Ser	Thr (1373)	FRAMESHIFT	homeobox	Human Gene Homologous to SPTREMBL-ID:O00503 CAUDAL- TYPE HOMEOBOX PROTEIN 2 - HOMO SAPIENS (HUMAN), 313 aa.	6.00E-118	13
1001	cg43929210	483	TCTGGCTCAGCA TGATGTTCCCTC T[G <i>gap</i>]GCCCTC AGCCTGCCACTA AAGAAATG	G	<i>gap</i>	Ala	Ala (1374)	FRAMESHIFT	hydroxysteroid	Human Gene SWISSPROT- ID:P51659 ESTRADIOL 17 BETA- DEHYDROGENASE 4 (EC 1.1.1.62) (17-BETA-HSD 4) (17-BETA- HYDROXYSTEROID DEHYDROGENASE 4) - HOMO SAPIENS (HUMAN), 736 aa.	0.00E+00	5
1002	cg44004587	1811	GCTTATTTTCGG TGTTGAATAAGA A[G <i>gap</i>]ACACTA AAAGCTCGATGC AATAATC	G	<i>gap</i>	Val	Val (1375)	FRAMESHIFT	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3.00E-123	
1003	cg41501665	156	CGCTTCTCCAAG GTGCTGGAGGA GG[C <i>gap</i>]GGCG GCCGCCGAGGA GGGCCTGCGC	C	<i>gap</i>	Ala	Gly (1376)	FRAMESHIFT	kinase	Human Gene Similar to TREMBL-NEW- ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa.	2.70E-76	

1004	cg41501665	184	CGGCCGCCGAG GAGGCCTGCG CGA[G/gap]CTGC AGCGAGCCGG CGGCTCTGCC	G	gap	Leu	Cys (1377)	FRAMESHIFT	kinase	Human Gene Similar to TREMBLNEW- ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa.	2.70E-76	
1005	cg41501665	202	TGCGCGAGCTG CAGCGCAGCCG GCG[G/gap]CTCT GCCACGAGGAC GTGGAGGCCG	G	gap	Leu	Ser (1378)	FRAMESHIFT	kinase	Human Gene Similar to TREMBLNEW- ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa.	2.70E-76	
1006	cg41501665	232	GCCACGAGGAC GTGGAGGCGCT GGC[C/gap]GCCA TCTACGAGGAGA AGGAGGCCT	C	gap	Ala	Pro (1379)	FRAMESHIFT	kinase	Human Gene Similar to TREMBLNEW- ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa.	2.70E-76	
1007	cg43939695	342	CAAGACTGAGAT CAATTGCCGGC GG[C/gap]CGGA CGATGGGAACC TCTTCCCCCT	C	gap	Pro	Arg (1380)	FRAMESHIFT	kinasere ceptor	Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa.	0.00E+00	15 (15q25)
1008	cg29023997	199	TCTGGATGGGAT GGAGCACCATG TG[C/gap]GCACC TGCATCCCCAAA GTGGAGCT	C	gap	Arg	Ala (1381)	FRAMESHIFT	kinasere ceptor	Human Gene SWISSPROT- ID:P36896 SERINE/THREONINE- PROTEIN KINASE RECEPTOR R2 PRECURSOR (EC 2.7.1.37) (SKR2) (ACTIVIN RECEPTOR-LIKE KINASE 4) (ALK-4) (ACTR-IB) - HOMO SAPIENS (HUMAN), 505 aa.	9.30E-280	12
1009	cg43983535	4377	CTCCAAACAGCT TCTTCACTTTTT [C/gap]AGAAGGG CTTCTGCAGCTA CCAACT	C	gap	Leu	Leu (1382)	FRAMESHIFT	laminin	Human Gene SWISSPROT- ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa.	0.00E+00	6 (6q22)

1010	cg42488873	480	TTCCCTTAAAT TGGTCAGCATAG T[G/gap]CCCCAT TTTGGGGCATCC TTCAGCT	G	gap	His	Thr (1383)	FRAMESHIFT	lipase	Human Gene SWISSPROT- ID:P54317 PANCREATIC LIPASE RELATED PROTEIN 2 PRECURSOR (EC 3.1.1.3) - HOMO SAPIENS (HUMAN), 469 aa.	9.80E-261	
1011	cg42488873	494	GTCAGCATAGTG CCCCATTTTGGG G[C/gap]ATCCTT CAGCTGGACAA GGGAAACA	C	gap	Cys	Ser (1384)	FRAMESHIFT	lipase	Human Gene SWISSPROT- ID:P54317 PANCREATIC LIPASE RELATED PROTEIN 2 PRECURSOR (EC 3.1.1.3) - HOMO SAPIENS (HUMAN), 469 aa.	9.80E-261	
1012	cg42488873	923	CACGCGGCCCC CCAGCCTCCTG CC[C/gap]CCTC CGCGGCCGTGT GCGCGCCCG	G	gap	Ala	Gly (1385)	FRAMESHIFT	lipase	Human Gene SWISSPROT- ID:P54317 PANCREATIC LIPASE RELATED PROTEIN 2 PRECURSOR (EC 3.1.1.3) - HOMO SAPIENS (HUMAN), 469 aa.	9.80E-261	
1013	cg43249083	2329	GGAGCAGCTCC AGGAGACGCTG CTG[C/gap]GGGC TCTTCGGGCTCT GGTGCTGAA	C	gap	Arg	Gly (1386)	FRAMESHIFT	nucl_rec pt	Human Gene SWISSPROT- ID:P20393 V-ERBA RELATED PROTEIN EAR-1 - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00	17 (17q11.2)
1014	cg43991048	6644	TCCTTCCTTCTT CTCTCTTTTTTTT C[gap]TGTTTTTT CTGCTTTATCCT CTTCT	C	gap	Glu	Lys (1387)	FRAMESHIFT	nucl_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	0.00E+00	17
1015	cg43919677	4055	GAAGAAAAGAAA GAATGCTACTAT A[A/gap]TCTCAAT GACGCCAGTCT CTGTGAT	A	gap	Asn	Ile (1388)	FRAMESHIFT	oncogen e	Human Gene SWISSPROT- ID:Q00918 LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP- 1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT) - RATTUS NORVEGICUS (RAT), 1712 aa.	0	2 (2p12)

1016	cg43997978	3546	CATCAGCTCACT GTAGATTACCTC T[G/gap]CTTCGT CAATGAGGGATT CCACGGA	G	gap	Ala	Glu (1389)	FRAMESHIFT	oncogen e	Human Gene SPTREMBL-ID:Q60875 LFC ONCOGENE - MUS MUSCULUS (MOUSE), 573 aa.	2.9E-244	1
1017	cg43916615	75	ATGACGGAATAT AAGCTGGTGGT GGT[gap]GGGC GCCGGCGGTGT GGCAAGAGT	T	gap	Val	Gly (1390)	FRAMESHIFT	oncogen e	Human Gene Similar to TREMBLNEW- ID:G332185 TRANSFORMING PROTEIN (P21 HAS) - HARVEY MURINE SARCOMA VIRUS, 241 aa.	3.1E-98	
1018	cg43916615	76	TGACGGAATATA AGCTGGTGGT GT[G/gap]GGCGC CGCGGTGTGG GCAAGAGTG	G	gap	Gly	Ala (1391)	FRAMESHIFT	oncogen e	Human Gene Similar to TREMBLNEW- ID:G332185 TRANSFORMING PROTEIN (P21 HAS) - HARVEY MURINE SARCOMA VIRUS, 241 aa.	3.1E-98	
1019	cg43916615	77	GACGGAATATA GCTGGTGGTGG TG[G/gap]GCGCC GGCGGTGTGG CAAGAGTGC	G	gap	Gly	Ala (1392)	FRAMESHIFT	oncogen e	Human Gene Similar to TREMBLNEW- ID:G332185 TRANSFORMING PROTEIN (P21 HAS) - HARVEY MURINE SARCOMA VIRUS, 241 aa.	3.1E-98	
1020	cg43069905	900	AGCTCCAGCAGT GACAGGTCATT TIC[gap]CCCCGC GTCCGCGTCATA CCGCATG	C	gap	Glu	Arg (1393)	FRAMESHIFT	protease	Human Gene Similar to SWISSPROT- ID:P25155 COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6) (STUART FACTOR) (VIRUS ACTIVATING PROTEASE) (VAP) - GALLUS GALLUS (CHICKEN), 475 aa.	1.3E-57	13
1021	cg43069905	904	CAGCAGTGACA GGTCATTCTCCC CC[gap]C/GCGTC CGCGTCATACC GCATGTGCA	gap	C	Ala	Ala (1394)	FRAMESHIFT	protease	Human Gene Similar to SWISSPROT- ID:P25155 COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6) (STUART FACTOR) (VIRUS ACTIVATING PROTEASE) (VAP) - GALLUS GALLUS (CHICKEN), 475 aa.	1.3E-57	13

1022	cg44028327	904	ATGCATACATCG A ATATTCAGCTAC G[A/gap]ATTGCT TCCTTCTCACAG AACTGTG	A	gap	Ile	Leu (1395)	FRAMESHIFT	proteasei nhib	Human Gene SWISSPROT- ID:P01042 KININOGEN, HMW PRECURSOR (ALPHA-2-THIOL PROTEINASE INHIBITOR) (CONTAINS: BRADYKININ) - HOMO SAPIENS (HUMAN), 644 aa.	0	3 (3q27)
1023	cg43940280	720	CCTCGAAGTCTG C CCTGGGCACAC AC[C/gap]ACATG CAGATTTTGGTG CTTTCCCA	C	gap	Gly	Val (1396)	FRAMESHIFT	ribosoma lprot	Human Gene Similar to SWISSPROT- ID:P49207 60S RIBOSOMAL PROTEIN L34 - HOMO SAPIENS (HUMAN), 116 aa.	7.6E-56	
1024	cg43974196	5050	GATTCAGGGCG C TGCTCTGGGGTGA AG[C/gap]CCACA GGGTTGAGAAA GCGAACCTC	C	gap	Pro	Pro (1397)	FRAMESHIFT	struct	Human Gene SWISSPROT- ID:Q02440 DILUTE MYOSIN HEAVY CHAIN, ISOFORM I (MYOSIN HEAVY CHAIN P190) (MYOSIN-V) - GALLUS GALLUS (CHICKEN), 1829 aa.	0	15 (15q21)
1025	cg43916919	1130	GAAGAAGACGC G CCTGGTTCTCTT GC[G/gap]CCACA GGCACCGGCTT CAGCTTCTC	G	gap	Ala	Gly (1398)	FRAMESHIFT	struct	Human Gene SWISSNEW-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP-G) - HOMO SAPIENS (HUMAN), 348 aa. pols:SWISSPROT-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP-G) - HOMO SAPIENS (HUMAN), 348 aa.	4.3E-188	2 (2cen)
1026	cg21428405	293	ATCTCTTCAGGG C GCGAGGTTCCG GT[C/gap]GCGCA GCGGAACGCGG TCGAGCTCG	C	gap	Asp	Thr (1399)	FRAMESHIFT	synthase	Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCIN AMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa.	2.2E-56	

1027	cg43336100	290	ATCATGCTGGAG AACTCGCAGATG A[G/gap]AGAGCG CATGCTGCTGCA AGCCACG	G	gap	Arg	Lys (1400)	FRAMESHIFT	tnf	Human Gene SWISSPROT- ID:P26022 PENTAXIN-RELATED PROTEIN PTX3 PRECURSOR (TUMOR NECROSIS FACTOR- INDUCIBLE PROTEIN TSG-14) - HOMO SAPIENS (HUMAN), 381 aa.	2.2E-207	3 (3q25)
1028	cg39517655	438	GGGGCCCTTAC TCGCTATGCTGC AA[G/gap]GGCCC CGGGCCCTTGGC TTCGGCCCGC	G	gap	Gly	Gly (1401)	FRAMESHIFT	transcript factor	Human Gene SWISSPROT- ID:Q14209 TRANSCRIPTION FACTOR E2F2 (E2F-2) - HOMO SAPIENS (HUMAN), 437 aa.	1.4E-237	1
1029	cg43954704	1391	CCCACTGGAAGT GGAGGCTCCAG TC[A/gap]AACCC CCCTCTGAGCTC CGAGGCAG	A	gap	Phe	Leu (1402)	FRAMESHIFT	transferase	Human Gene Similar to SPTREMBL- ID:Q29121 UDP- GALNAC:POLYPEPTIDE ALFA-1, O N- ACETYLGALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	1.1E-68	2
1030	cg43986426	1227	GCGGACAGTCG CCCTAAGCAGTG CA[A/gap]GGTGT CTTGAGCCCTAT GGTGGCCA	A	gap	Arg	Gly (1403)	FRAMESHIFT	ubiquitin	Human Gene SWISSPROT- ID:P41226 UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG (D8) - HOMO SAPIENS (HUMAN), 1011 aa.	0	1
1031	cg43917221	2853	GAATGTCATCC ACGGTATTTTTT [T/gap]CAGTTTTA GTTTGACCAAAG CTTTA	T	gap	Lys	Lys (1404)	FRAMESHIFT	UNCLASSIFIED	Human Gene SWISSNEW- ACC:Q13563 POLYCYSTIN 2 (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE TYPE II PROTEIN) (POLYCYSTWIN) (R48321) - Homo sapiens (Human), 968 aa.	0	4 (4q21)
1032	cg43918356	2640	ATGTCATCTTCA TCTAGAAACGCC C[gap/A]TCACGG AAATGGAATTGC TGCCAGA	gap	A	Arg	Met (1405)	FRAMESHIFT	UNCLASSIFIED	Human Gene SPTREMBL- ACC:O75176 KIAA0692 PROTEIN - HOMO SAPIENS (HUMAN), 783 aa (fragment).	0	12

1033	cg43918446	2812	CTTCCACATG ACTTGTTACATT C[C/gap]GACCAC TGGGACCACTC GGTGAGCT	C	gap	Ser (1406)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	
1034	cg43927750	2857	TAAAAGTTATTCT CCAATGGTGATT [G/gap]GGCAAGC CCTGCCTCCTGT ATTCTT	G	gap	Pro (1407)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q13496 MYOTUBULARIN - Homo sapiens (Human), 603 aa.	0	X (Xq28)
1035	cg43961075	1344	GGGTAGGATTG CTCATTTCAGGG CAIG/gap]CTGTC GCAAGCATCTCC CACCCCGT	G	gap	Ser (1408)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P49746 THROMBOSPONDIN 3 PRECURSOR - Homo sapiens (Human), 956 aa.	0	1
1036	cg43961763	1192	CATCTAGGTCAA CAGGAAGGTCA AG[C/gap]TCCCG CTCCGGTTCCAC TGATCCAT	C	gap	Asp (1409)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P13521 SECRETAGRANIN II PRECURSOR (SGII) (CHROMOGRANIN C) - Homo sapiens (Human), 617 aa.	0	2
1037	cg43968223	2979	GTTCTGTTCTTG TAGCGCTTTCTG C[G/gap]CTGCAG CATGATCTGAAG CTTGTTG	G	gap	Ala (1410)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O60342 KIAA0602 PROTEIN - HOMO SAPIENS (HUMAN), 962 aa (fragment).	0	14
1038	cg43980727	2673	CCCTCCAGGTA GAGGCCTAGGA AGG[C/gap]CCCCA GAACTGAAGCC GAAGCGCTGG	C	gap	Pro (1411)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P38432 P80-COILIN - Homo sapiens (Human), 576 aa.	0	17
1039	cg43999667	3941	TTCTGTTTTGTC AGGACTTTTTTTT [T/gap]CTACAAG TTGTTTTTCTGG GATCAC	T	gap	Glu (1412)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O60281 KIAA0530 PROTEIN - HOMO SAPIENS (HUMAN), 1563 aa (fragment).	0	6

1040	cg44022781	3927	GTATCAAAAGTGC TCTTTCCAACTTT [T/gap]GGAGGCC CCATCACCACCTA CCGGTA	T	gap	Pro (1413)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14692 KIAA0187 PROTEIN - HOMO SAPIENS (HUMAN), 1282 aa.	0	
1041	cg44919370	571	CGTGGACTTTTC CGAGGATGACC CC[C/gap]TGGAG GCCACTGTCCAT TGGGCCCC	C	gap	Leu (1414)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O60624 CLASS I CYTOKINE RECEPTOR - HOMO SAPIENS (HUMAN), 636 aa.	0	19
1042	cg44932924	2612	TCTACAACCAGA GCCAGGAATTAC A[G/gap]ACGAAG CTGGAGGACTG CAGGAACA	G	gap	Thr (1415)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q92574 HAMARTIN (MYELOBLAST KIAA0243) - HOMO SAPIENS (HUMAN), 1164 aa.	0	9
1043	cg43991434	1167	GGGGTGCAAGG GCCCTGGGGAA ATA[G/gap]TCCT GCTGCACCATGT GGTTCAGCG	G	gap	Asp (1416)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:P46060 RAN-GTPASE ACTIVATING PROTEIN 1 - Homo sapiens (Human), 587 aa.	1.7E-304	22
1044	cg44931278	1264	CCTCCTCCAGG GAAGCACTGGC CAG[G/gap]TCCT GCAGGTAGGC CACTTCTGCA	G	gap	Asp (1417)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q15830 MUTY HOMOLOG - HOMO SAPIENS (HUMAN), 535 aa.	4.5E-280	1
1045	cg43949042	427	CACAGCTGCGTT GCCATAGTTGCC CT[gap]GGAAAA AGCGGCCACG AACCAGGC	T	gap	Arg (1418)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75907 ACAT RELATED GENE PRODUCT 1 - HOMO SAPIENS (HUMAN), 488 aa.	6.10E-268	
1046	cg43972066	2313	TAAATTGACTTT TCTCATGTAAAA A/gap]TGTCTAAT GCGATGTATTG GTAAT	A	gap	His (1419)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O60747 PUTATIVE G-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 562 aa (fragment).	4.10E-221	10

1047	cg43955639	723	GGGGGTACTGG GGACCTCGTCT GTT[G/gap]GGTT CCCCTCCTCCAG GGTAGCGGC	G	gap	Pro	Gln (1420)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O15417 CAGL79 - HOMO SAPIENS (HUMAN), 413 aa (fragment).	2.80E-215	
1048	cg43955639	725	GGGTACTGGGG ACCTCGTCTGTT GG[G/gap]TTCCC CTCCTCCAGGGT AGCGGCTC	G	gap	Asn	Asn (1421)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O15417 CAGL79 - HOMO SAPIENS (HUMAN), 413 aa (fragment).	2.80E-215	
1049	cg43965656	391	CTGCCTATTCTG AACCAGCCCAACA TTC[gap]TGAGAT TGTTGCCAATGC CCGAGGT	C	gap	Ser	Leu (1422)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q99541 ADIPOPHILIN - HOMO SAPIENS (HUMAN), 437 aa (fragment).	7.20E-210	
1050	cg43944615	2370	TACATGGCACAG AGGAAGAAGCG CA[G/gap]CACGG CGCTGCAGTTCA CGTCCACC	G	gap	Leu	Cys (1423)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O14877 FRPHE - HOMO SAPIENS (HUMAN), 346 aa.	1.30E-192	
1051	cg43323906	334	CTCTGGTGCTGC TCCTCTGAAGAT TTC[gap]AAGCTT ATTCAATGAGA CTGCAGA	C	gap	Gln	Lys (1424)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P42081 T LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2 ANTIGEN) (CTLA-4 COUNTER- RECEPTOR B7.2) (B70) (FUN-1) (BU63) - Homo sapiens (Human), 329 aa.	1.80E-174	
1052	cg44004690	251	GAGGAGGAGGA GGTGGAGGAGG AGG[A/gap]GGGA GAAGAGGATGTT TTCACCGAG	A	gap	Glu	Gly (1425)	FRAMESHIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74892 KIAA0869 PROTEIN - HOMO SAPIENS (HUMAN), 888 aa (fragment).	2.50E-161	

1053	cg44004690	402	ACCGGAGAGTG GGCACCCCGTC CCA[G/gap]GGG CCATTTCTTCGA GGGAGCACCA	G	gap	Gly	Gly (1426)	FRAMESHIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74892 KIAA0869 PROTEIN - HOMO SAPIENS (HUMAN), 888 aa (fragment).	2.50E-161	
1054	cg43957283	322	TCGAGGGTGAC CACAGCCCCAG AGG[G/gap]CCG CAGCACAGCGC AGGGGGTGGCG	G	gap	Pro	Pro (1427)	FRAMESHIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD27734 CGI-25 PROTEIN - HOMO SAPIENS (HUMAN), 301 aa.	1.40E-160	
1055	cg43329741	336	GCTCTACCTGG GCTACACCCCG CAG[G/gap]CGG CCCGTGAAGTG CGCATCATGCA	G	gap	Ala	Arg (1428)	FRAMESHIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD39906 FH1/FH2 DOMAIN- CONTAINING PROTEIN FHOS - HOMO SAPIENS (HUMAN), 1164 aa.	6.70E-159	
1056	cg44010310	501	TTTGGTTGAGATG CATGAATTTTTTT [gap/T]CTCTATTG CTGCTTGAAAT TTACA	gap	T	Lys	Lys (1429)	FRAMESHIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA32101 BCAP - HOMO SAPIENS (HUMAN), 331 aa.	1.30E-155	13
1057	cg39729127	981	GCTCTCTCTTT ATTGGTAACCG T[gap/T]GGTGGC CACGAGTCATAC AGGGAAA	gap	T	Val	Val (1430)	FRAMESHIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD42876 NY-REN-45 ANTIGEN - HOMO SAPIENS (HUMAN), 815 aa.	3.00E-152	1
1058	cg43135797	861	AGATCTGTCTCC CCGGAGACCCG GA[G/gap]CCGCT GGCCATTGCAG AAGGCGCCC	G	gap	Leu	Ser (1431)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O14732 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE 2 (EC 3.1.3.25) (IMP 2) (INOSITOL MONOPHOSPHATASE 2) (MYO- INOSITOL MONOPHOSPHATASE A2) - Homo sapiens (Human), 288 aa.	1.60E-150	18

1059	cg43965796	1704	ATCACTGTTGAT GCTCTGGGCCA CG[C/gap]CAGG GTA CTGGATCTT CATGGCCAC	C	gap	Gly	Ala (1432)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment).	9.00E-148	1
1060	cg43965796	1705	TCACTGTTGATG CTCTGGGCCAC GC[C/gap]AGGGT ACTGGATCTTCA TGGCCACC	C	gap	Gly	Ala (1433)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment).	9.00E-148	1
1061	cg42907867	1100	AGGGCCACGGG GTGGGCCACGGG GGC[C/gap]GGG CCATTCCAGTG GCTCCTTGTC	C	gap	Arg	Arg (1434)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99769 HYPOTHETICAL 26.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 255 aa.	1.10E-140	1
1062	cg43922710	126	TCTACCCAGCTA AATACACATTAT G[G/gap]CATTTA GCAAACTAACTT ACAAAGTC	G	gap	Ala	His (1435)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA74897 KIAA0874 PROTEIN - HOMO SAPIENS (HUMAN), 601 aa (fragment).	4.90E-140	
1063	cg43303845	1073	GCAGGAACGCC TGGATCGGGAG AGG[C/gap]AAGA AAGACAAGAACG AGAGAGGCT	C	gap	Gln	Lys (1436)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q93263 AVENA - GALLUS GALLUS (CHICKEN), 550 aa.	1.90E-138	
1064	cg43973762	430	ATAACAGAAAGC AAGAGAAAGTGTG A[G/gap]AACTCT GAAAGAAAGAGT TCAAAAG	G	gap	Arg	Lys (1437)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14777 RETINOBLASTOMA-ASSOCIATED PROTEIN HEC - HOMO SAPIENS (HUMAN), 642 aa.	2.20E-137	
1065	cg43918679	411	TCACAGATATCT CCATTGGCCAGG A[G/gap]ATGCCC AGCCTGGAGGT GATCACGC	G	gap	Met	Cys (1438)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q43822 28.3 KD PROTEIN C21ORF2 (C21ORF- HUMF09G8.5) (YF5/A2) - Homo sapiens (Human), 256 aa.	3.00E-131	21

1066	cg38059286	503	GCCGCTCCCTCT TCTCACTGAAGC A[G/gap]ATCTTC CAGGAGGACAA AGACCTGG	G	gap	Ile	Ser (1439)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD39906 FH1/FH2 DOMAIN-CONTAINING PROTEIN FHOS - HOMO SAPIENS (HUMAN), 1164 aa.	4.00E-129	
1067	cg42549778	1014	ACTGTCACTTCC CTGCTGCAGGG CA[G/gap]CCCC ACCTGTGAGTG GCTCGAGCC	G	gap	Ser	Thr (1440)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD29690 PUTATIVE ZINC FINGER TRANSCRIPTION FACTOR OVO1 - MUS MUSCULUS (MOUSE), 267 aa.	3.70E-126	
1068	cg44921277	516	CCCTGATCATCC TCATCGTGGAGC T[G/gap]TGC GGG CTCCAGGCCCG CTTCCCCC	G	gap	Cys	Ala (1441)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O35682 MYELOID UPREGULATED PROTEIN - Mus musculus (Mouse), 296 aa.	1.70E-120	
1069	cg44921277	518	CTGATCATCCTC ATCGTGGAGCT GT[G/gap]CGGGC TCCAGGCCCGC TTCCCCCTG	G	gap	Cys	Ser (1442)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O35682 MYELOID UPREGULATED PROTEIN - Mus musculus (Mouse), 296 aa.	1.70E-120	
1070	cg42530218	327	GATTTAATACAC AGCAGCAGCAG CA[gap/G]AACTA CATTAGGTGGTC TCTTCAGT	gap	G	Gln	Gln (1443)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P70582 NUCLEOPORIN P54 - RATTUS NORVEGICUS (RAT), 510 aa.	2.00E-118	
1071	cg42530218	329	ATTTAATACACA GCAGCAGCAGC AA[A/gap]CTACA TTAGGTGGTCTC TTCAGTCA	A	gap	Thr	Leu (1444)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P70582 NUCLEOPORIN P54 - RATTUS NORVEGICUS (RAT), 510 aa.	2.00E-118	
1072	cg43325007	979	AGGATACCCCC GAGGAAGGCCG CCA[G/gap]GAAT GCGTGTGCTGG GTAGGTCTTG	G	gap	Leu	Trp (1445)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD43195 PEROXISOMAL MEMBRANE PROTEIN PMP 24 - HOMO SAPIENS (HUMAN), 212 aa.	4.80E-110	20

1073	cg43981269	776	GGCCTACGGCG CCTACGCTCAG GCA[C/gap]TGAT GCAGCAGCAAG CGGCCCTGAT	C	gap	Leu	End (1446)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q91579 RIBONUCLEOPROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 462 aa.	4.50E-105	
1074	cg43250166	166	AGGTGGCCCTC ACACCCAGTGCT GT[G/gap]CTGCG CGGAGGGCTGT ACTGAAGGT	G	gap	Ala	Asp (1447)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43382 HYPOTHETICAL 146.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 1296 aa.	3.30E-102	2
1075	cg43982164	778	CTGCGGGGGT GCTCATCCTGGA CA[gap/C]ATTCA CCTGCCTCCTAT GTCTTCCA	gap	C	Asn	Thr (1448)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15194 HYA22 - HOMO SAPIENS (HUMAN), 340 aa.	1.00E-90	
1076	cg43980889	812	TTAAATATAGAC AAGTGGACCAT TT[gap]GCCTCA AATTCACAGGAG CCAGCAT	T	gap	Ala	Pro (1449)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	4.50E-89	
1077	cg43970119	832	GTGGCCATTGGT GAGACATCCATC A[A/gap]TATTGC AAACCAAAAGTT TTATTTC	A	gap	Ile	Met (1450)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88719 CMP-N- ACETYLNEURAMINIC ACID SYNTHETASE (EC 2.7.7.43) (ACYLNEURAMINATE CYTIDYLTRANSFERASE) (CMP- SIALATE PYROPHOSPHORYLASE) (CMP-SIALATE SYNTHASE) - MUS MUSCULUS (MOUSE), 432 aa.	1.00E-82	12
1078	cg44030987	447	TCGGCATGTTGA GTGGAACAGTTG T[A/gap]TTTACTT GAATTCCAATCT CCTTCT	A	gap	Tyr	Thr (1451)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA76495 TYPE II MEMBRANE PROTEIN SIMILAR TO CD69 - HOMO SAPIENS (HUMAN), 149 aa.	1.90E-81	

1079	cg43320682	665	GGTGGCTCAGG GGCTGGGGGAG GCT[C/gap]CCCT GGGCTTCAGA CAGCACATAG	C	gap	Glu	Ser (1452)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45773 HYPOTHETICAL 18.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 162 aa (fragment).	6.60E-81	
1080	cg25255686	366	AAGGCACCATCA AGTCGGCGGTG GC[C/gap]ITTCGG GCATCTCCTTGC CGAGGGTA	C	gap	Phe	Ser (1453)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB39700 CONSERVED HYPOTHETICAL PROTEIN - STREPTOMYCES COELICOLOR, 384 aa.	2.10E-77	
1081	cg43988975	371	CTCCTCCTGACC GAGTGGGCCGG CA[C/gap]GAGCT TGAATCGTCAT TGGAGATG	G	gap	Glu	Ser (1454)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P50606 MAGO NASHI PROTEIN HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 146 aa.	8.00E-76	
1082	cg39523553	670	CACTGGTATGCA CGGCGCGTCT CC[G/gap]CAGTG TGAGGTCTGCC CGATCCGGG	G	gap	Gln	Ser (1455)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.20E-75	
1083	cg43951096	2953	CTCCCTCCTGG GTATCTGCATCT TC[gap/A]AAAT CTCCTTCTTGGT TTTCATCC	gap	A	Glu	End (1456)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa.	2.00E-71	17
1084	cg42831353	806	GGACACAGGCT GCGGTGTAAGC CCG[C/gap]GTCA CCGCCGGCACC TGCAGGAACT	C	gap	Thr	Thr (1457)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD37863 PUTATIVE NADH OXIDOREDUCTASE COMPLEX I SUBUNIT - CAENORHABDITIS ELEGANS, 237 aa.	1.30E-67	22

1085	cg44938009	688	AATACTCCGTGC AGCGAGTGCCT CA[G/gap]CTCCG TGAAGAAATTTGA TCAAGGTC	G	gap	Leu	Ser (1458)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O43182 RHO-GTPASE- ACTIVATING PROTEIN 6 (RHO-TYPE GTPASE-ACTIVATING PROTEIN RHO GAPX-1) - Homo sapiens (Human), 587 aa.	5.80E-66	X
1086	cg43054992	315	CAAAATCACAGC TGAAGAAATGTA T[G/gap]ATATATT TGGGAAATATGG ACCTAT	G	gap	Asp	Ile (1459)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34105 CGI-110 PROTEIN - HOMO SAPIENS (HUMAN), 125 aa.	4.60E-64	2
1087	cg39516123	928	CCTGGGGCTCA CCAAGGCAACCT GG[C/gap]CTCCG GTCTTCATAGCA ATGCAATA	C	gap	Ala	Ala (1460)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa.	5.10E-62	
1088	cg43983590	713	GGAGGAGCCAG GCGAGCACACC CCC[C/gap]TGTT GGCCCCCTGCCA CGGCCCCAGCC	C	gap	Leu	Cys (1461)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q19498 SIMILAR TO MELIBIOSE CARRIER PROTEIN - CAENORHABDITIS ELEGANS, 501 aa.	1.50E-60	
1089	cg44128084	499	CGGCGGCGCAT GCTCGACGTTCT GG[C/gap]GTCTG TCGACGAGTTGC CGGTGCAA	C	gap	Ala	Gly (1462)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa.	1.70E-59	
1090	cg44128084	524	CGTCTGTCGAC GAGTTGCCGGT GCA[A/gap]CGCT GGAGCTGCGAC GGGATCCTGG	A	gap	Arg	Ala (1463)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa.	1.70E-59	

1091	cg43976473	931	GGCCCTGTGCTT GGAGCCGTGGG CTC[<i>gap</i>]CGTAG CCCGAGTGATAA GCCATGGC	C	<i>gap</i>	Gly	Glu (1464)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O35946 HYPOTHETICAL 14.9 KD PROTEIN - RATTUS NORVEGICUS (RAT), 137 aa.	3.50E-59	11
1092	cg40309770	385	TTCCGGCCGCC GCGTCCAGGC TCG[C/ <i>gap</i>]CCGC TGAGGTCGTTCA TGACCCCGC	C	<i>gap</i>	Gly	Gly (1465)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q60870 POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106) - Mus musculus (Mouse), 185 aa.	4.10E-56	
1093	cg42725664	184	AGATAGCTGAGA ATATTCTGCGCA A[G/ <i>gap</i>]CCTCAC AGCTTGTTTCCT GGCAGCC	G	<i>gap</i>	Leu	Leu (1466)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA74896 KIAA0873 PROTEIN - HOMO SAPIENS (HUMAN), 466 aa (fragment).	1.5E-51	
1094	cg39380052	497	ATGAGATCGACG CCTTGCGCGGC CG[C/ <i>gap</i>]GGCGT AGACATTCCGCA CCCGCTCA	C	<i>gap</i>	Gly	Ala (1467)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB42016 PUTATIVE ADENYLOSUCCINATE SYNTHETASE - STREPTOMYCES COELICOLOR, 427 aa.	1.3E-50	
1095	cg44928804	1181	CTCTCAATCATG CCGCTTTAGAGA A[T/ <i>gap</i>]GCAACA TGGGCAACCTG ATTTGTGA	T	<i>gap</i>	Cys	Ala (1468)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P21589 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO- NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN) - Homo sapiens (Human), 574 aa.	9.1e-313	6 (6q14)